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Db      1  MVLRLVILLLSNAAAGGCGYGNPLNKYIRHREGSLYNVDLSHOKHRAKRAVSHEDQFL 60
Oy      61  RUDFHAGRHFNLMKRDTSLSDFEKFVETSNKVLDYDTSHTYGHITGEGSLAMGLL 120
Db      61  RUDFHAGRHFNLMKRDTSLSDFEKFVETSNKVLDYDTSHTYGHITGEGSLAMGLL 120
Oy      121  MEDLKSSRLVVAHFMEFPAERYIKDRTLPHFSVYIHEDDINYPHKYPOGGCADHSVFE 180
Db      121  DGRFGFOTGCTFYFVEPAERYIKDRTLPHFSVYIHEDDINYPHKYPOGGCADHSVFE 180
Oy      181  RMKRYOMTGVEEVTOIPOEHAANGPELLRKRRTNSAEKNCOLYOTDHLFPKYGTRE 240
Db      181  RMKRYOMTGVEEVTOIPOEHAANGPELLRKRRTNSAEKNCOLYOTDHLFPKYGTRE 240
Oy      241  AVIAOISSHAKAIDITYOTDTSFGIRNISFWVKRIRINTTADKDPINPRFPNIGVEKF 300
Db      241  AVIAOISSHAKAIDITYOTDTSFGIRNISFWVKRIRINTTADKDPINPRFPNIGVEKF 300
Oy      301  LEINSEONHDDYCLAYVFTDRDPDGVGLAMVGAPOSSGGICSKSLYSDGKKSLNT 360
Db      301  LEINSEONHDDYCLAYVFTDRDPDGVGLAMVGAPOSSGGICSKSLYSDGKKSLNT 360
Oy      361  GIITVQNTGSHVPPKVSHTTFAHEVGHNGSPHDSGCTPGESEKNLGOKEKNYIMYAR 420
Db      361  GIITVQNTGSHVPPKVSHTTFAHEVGHNGSPHDSGCTPGESEKNLGOKEKNYIMYAR 420
Oy      421  ATSGDKLNNKFSCLSRINISQYLEKKRNKCFVESGOTICGNGVYEGEEDCGYSQOCK 480
Db      421  ATSGDKLNNKFSCLSRINISQYLEKKRNKCFVESGOTICGNGVYEGEEDCGYSQOCK 480
Oy      481  DECCPDANOPRGKCKLKPKQCSPOGCTAOCFAKSKSEKCRDSDCARBESICNGFT 540
Db      481  DECCPDANOPRGKCKLKPKQCSPOGCTAOCFAKSKSEKCRDSDCARBESICNGFT 540
Oy      541  ALCPASDPKPFNTDGNHRTQVCIINGOCASICEKYGLEECCTASDGDDELCHVCCMK 600
Db      541  ALCPASDPKPFNTDGNHRTQVCIINGOCASICEKYGLEECCTASDGDDELCHVCCMK 600
Oy      601  KMDSTCAGTSGVQMSHNSGRTTTLQPSGPCNDPFGYCDVYMRCLYDADGPIARLKA 660
Db      601  KMDSTCAGTSGVQMSHNSGRTTTLQPSGPCNDPFGYCDVYMRCLYDADGPIARLKA 660
Oy      661  IFSPELVENIAEWIVAHMAVLLMGLALIMLMAFGIKICSVTPSPSNKLPPLPGLGTL 720
Db      661  IFSPELVENIAEWIVAHMAVLLMGLALIMLMAFGIKICSVTPSPSNKLPPLPGLGTL 720
Oy      721  KRRRPPQIQOPORPRESYOMGNMR 748
Db      721  KRRRPPQIQOPORPRESYOMGNMR 748

RESULT 2
010741  PRELIMINARY: PRT: 748 AA.
010741  01-NOV-1996 (TREMblrel. 01, Created)
01-NOV-1996 (TREMblrel. 01, Last sequence update)
01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE  DISTINTEGRIN-METALLOPROTEASE PRECURSOR (EC 3.4.24.-) (MYELIN-ASSOCIATED
DE  METALLOPROTEINASE) (MADM).
OS  Bos taurus (Bovine).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC  Bovidae; Bovinae; Bos.
OX  NCBI_TaxID=9913;
RN  (1)
RP  SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC  TISSUE=BRAIN;
RC  MEDLINE=96276398; PubMed=8694785;
RA  Howard L., Lu X., Mitchell S., Griffiths S., Glynn P.;
RT  "Molecular cloning of MADM: a catalytically active mammalian
RT  distinct integrin metalloprotease expressed in various cell types."

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RL  Blochem. J. 317:45-50(1996).
CC  -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC  -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN BRAIN. AT LOWER
CC  LEVELS IN KIDNEY, SPLEEN, LUNG AND HEART.
CC  -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2C (ZINC
CC  METALLOPROTEASE).
CC  -1- SIMILARITY: HIGH, IN THE MIDDLE REGION, TO DISTINTEGRINS.
DR  EMBL: Z21961; CAAT9973.1; -.
DR  HSSP: P18619; LEVL.
DR  MEROPS: M12.210; -.
DR  InterPro: IPR001762; Distintegrin.
DR  InterPro: IPR001590; Repeptolysin.
DR  InterPro: IPR000130; Zn_MPeptidase.
DR  Pfam: PF00200; distintegrin.1.
DR  Pfam: PF01421; Repeptolysin.1.
DR  SMART: SM00050; Disin.1.
DR  PROSITE: PS50215; ADAM_MERPO.1.
DR  PROSITE: PS50214; DISTINTEGRIN.2; 1.
DR  PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN.1.
KW  Integrin; Hydrolase; Metalloprotease; Transmembrane; Zinc; Signal;
KW  Glycoprotein.
FT  SIGNAL 1..19
FT  PROPEP 20..213
FT  CHAIN 214..455
FT  CHAIN 456..550
FT  DOMAIN 20..672
FT  TRANSMEM 673..696
FT  DOMAIN 697..748
FT  ACT_SITE 384..384
FT  METAL 383..383
FT  METAL 387..387
FT  METAL 393..393
FT  CARBOHYD 267..267
FT  CARBOHYD 278..278
FT  CARBOHYD 439..439
FT  CARBOHYD 551..551
SQ  SEQUENCE 748 AA; 84188 MW; 202E29830611F9E1 CRC64;

Query Match 94.2%; Score 3852; DB 6; Length 748;
Best Local Similarity 93.7%; Pred. No. 0;
Matches 701; Conservative 20; Mismatches 27; Indels 0; Gaps 0;

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: April 1, 2002, 15:11:59; Search time 98.78 Seconds

(without alignments)  
1107.630 Million cell updates/sec

Title: US-09-871-388-4

Sequence: 1 MYLLRVLILLLSMAAGMCGQ.....IQQPQRRPRESYQMGHMRR 748

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

SPTREMBL\_17:\*

- 1: sp.archaea:\*
- 2: sp.bacteria:\*
- 3: sp.fungi:\*
- 4: sp.human:\*
- 5: sp.invertebrate:\*
- 6: sp.mammal:\*
- 7: sp.mhc:\*
- 8: sp.organelle:\*
- 9: sp.phage:\*
- 10: sp.plant:\*
- 11: sp.protoct:\*
- 12: sp.virus:\*
- 13: sp.vertebrate:\*
- 14: sp.unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3959	96.8	748	4	014672	014672 homo sapien
2	3852	94.2	748	6	010741	010741 bos taurus
3	3804.5	93.0	749	11	035598	035598 mus musculu
4	3333.5	81.5	691	4	010742	010742 homo sapien
5	2920	71.4	544	11	010743	010743 ratcus norv
6	1452	35.5	1238	5	09VDM9	09VDM9 drosophila
7	1451	35.5	1236	5	09NKF9	09NKF9 drosophila
8	1450.5	35.5	1239	5	094902	094902 drosophila
9	1350.5	32.9	922	5	046354	046354 caenorhabdl
10	1345.5	33.9	1537	5	09VARI2	09VARI2 drosophila
11	707	17.3	162	13	042568	042568 xenopus lae
12	475	11.6	686	5	094316	094316 caenorhabdl
13	409.5	10.0	600	13	09PVK7	09PVK7 najia najia (
14	406	9.9	75	6	077633	077633 sus scrofa
15	392.5	9.6	845	11	061072	061072 mus musculu
16	386	9.4	819	4	013443	013443 homo sapien
17	372.5	9.1	914	13	012960	012960 xenopus lae
18	365.5	8.9	873	13	042595	042595 xenopus lae
19	363	8.9	610	13	09DGB9	09DGB9 crocatus at

20	356	8.7	604	13	09PT48	09PT48 atractaspis
21	356	8.7	735	11	060411	060411 cavia porce
22	352.5	8.6	620	11	042138	042138 agkistrodon
23	349.5	8.5	616	13	090495	090495 echis carin
24	349.5	8.5	728	4	09B211	09B211 homo sapien
25	338.5	8.3	617	13	090499	090499 echis pyram
26	337	8.2	606	13	098UF9	098UF9 bothrops ja
27	334	8.2	920	11	035674	035674 mus musculu
28	333	8.1	609	13	036M5	036M5 agkistrodon
29	329	8.0	419	13	092043	092043 crocatus at
30	327.5	8.0	505	13	073795	073795 agkistrodon
31	327.5	8.0	918	4	09H013	09H013 homo sapien
32	327.5	8.0	918	4	09B2L5	09B2L5 homo sapien
33	325.5	8.0	609	13	090282	090282 crocatus at
34	322	7.9	1569	5	09VFH0	09VFH0 drosophila
35	318.5	7.8	829	11	09R1V7	09R1V7 mus musculu
36	318	7.8	857	4	09DHP2	09DHP2 homo sapien
37	315.5	7.7	832	4	075077	075077 homo sapien
38	315	7.6	610	13	09Y120	09Y120 agkistrodon
39	311	7.6	549	13	090500	090500 echis pyram
40	310.5	7.6	487	13	092119	092119 trimeresuru
41	310.5	7.6	760	11	09D4F4	09D4F4 mus musculu
42	309	7.6	610	13	093523	093523 bothrops ja
43	308.5	7.5	903	11	061824	061824 mus musculu
44	307	7.5	739	4	09Y307	09Y307 homo sapien
45	303.5	7.4	481	13	057413	057413 trimeresuru

## ALIGNMENTS

RESULT 1

014672 PRELIMINARY; PRT; 748 AA.

AC 014672:

DT 01-JAN-1998 (TREMBlrel. 05, Created)

DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE ADAM10.

GN ADAM10.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_TaxID:9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97450992; PubMed=9305925;

RA Rosenthal M.S., Ko S.C., Long D.L., Brewer M.T., Rosenzweig B.,

RA Hedl E., Anderson H., Pyle S.M., Moreland J., Meyers M.A., Kono T.,

RA Lyons D., Lichenstein H.S.;

RT "Identification and characterization of a pro-tumor necrosis factor-

RT alpha-processing enzyme from the ADAM family of zinc

RT metalloproteases.";

RL J. Biol. Chem. 272:24588-24593(1997).

RL EMBL: AF009615; AAC51766.1; -

DR HSSP; P18619; 1FVL

DR InterPro; IPR001762; Disintegrin.

DR InterPro; IPR001590; Reptolysin.

DR InterPro; IPR000130; Zn\_MTPeptidse.

DR Pfam; PF00200; disintegrin; 1.

DR Pfam; PF01421; Reptolysin; 1.

DR SMART; SM00050; DISTR; 1.

DR PROSITE; PSS0215; ADAM\_MPRO; 1.

DR PROSITE; PSS0214; DISINTEGRIN\_2; 1.

DR PROSITE; PSS0142; ZINC\_PROTEASE; UNKNOWN; 1.

SQ SEQUENCE 748 AA; 84142 MW; 0881655B17022A71 CRC64;

Query Match 96.8%; Score 3959; DB 4; Length 748;

Best Local Similarity 96.9%; Pred. No. 0;

Matches 725; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 1 MYLLRVLILLLSMAAGMCGQYGNPLNKYTRHYEGLSYNDLSLHQKHQRAKRAVSHEDQFL 60

DR PROSITE: PS00214; DISINTEGRIN 2; 1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
 KM Integrin.  
 FT NON\_TER  
 SQ SEQUENCE 691 AA; 77632 MW; 8B43698P24B6B292 CRC64;

Query Match 81.5%; Score 3333.5; DB 4; Length 691;  
 Best Local Similarity 88.9%; Pred. No. 8.1e-265;  
 Matches 614; Conservative 7; Mismatches 19; Indels 51; Gaps 1;

QY 109 GEGSGIAMLMLLMEDLKSSRLVVAHMFPAEYIKDRLPHSHYIHEDIN-----162  
 DB 1 GEGSGFSHOSVIDGRFESGDTQPGGTVEPAERYIKDRLPHSHYIHEDISRLKLR 60  
 QY 163 -----YPAKYGPGGCAHDS 177  
 DB 61 LKRLMSLELMTSCDPCALLHSMKKAIVNSHCLYFKDFMGSEFITYPHKYGPGGCAHDS 120  
 QY 178 VERMRKYMGTVEEVTOIQPOEHAANGPELLKRTKTSNAEKNTQOLYIQDHLFFKYG 237  
 DB 121 VERMRKYMGTVEEVTOIQPOEHAANGPELLKRTKTSNAEKNTQOLYIQDHLFFKYG 180  
 QY -238 TEAVIAIOISSHVAIDITYQTDFSGIRNISFMVRIRINTADEKPTNFRPNIGV 297  
 DB 181 TEAVIAIOISSHVAIDITYQTDFSGIRNISFMVRIRINTADEKPTNFRPNISV 240  
 QY 298 EKFLNESEONHDDYCLAYVETDREDPDGVLGLAWGAPSGSGGICEKSKLYSGKKKS 357  
 DB 241 EKFLNESEONHDDYCLAYVETDREDPDGVLGLAWGAPSGSGGICEKSKLYSGKKKS 300  
 QY 358 LMTGIIYQVNGSHVPRKVSHTFAHEVGHNGSPHDSCTECTPEESKMLGQKENGNYIM 417  
 DB 301 LMTGIIYQVNGSHVPRKVSHTFAHEVGHNGSPHDSCTECTPEESKMLGQKENGNYIM 360  
 QY 418 YVARATSGDKLNNKFSCLISINISQVLEKRNKCFPESGQPICGNKMVQEGECGCGSD 477  
 DB 361 YVARATSGDKLNNKFSCLISINISQVLEKRNKCFPESGQPICGNKMVQEGECGCGSD 420  
 QY 478 QCKDCCCDANQPSGRCKKLPKQKQSPSCQCTAQAQAFKSKSEKCRDSDSCAREGICN 537  
 DB 421 QCKDCCCDANQPSGRCKKLPKQKQSPSCQCTAQAQAFKSKSEKCRDSDSCAREGICN 480  
 QY 538 GFTALCPASDPKPNFTDCNRRHTQVINGCAGSICEKYGLEECTCASSGKDKDELCHVC 597  
 DB 481 GFTALCPASDPKPNFTDCNRRHTQVINGCAGSICEKYGLEECTCASSGKDKDELCHVC 540  
 QY 598 CCKKNDPSTCASTSVQMSRHFSGRTITLQPSGPCNDFGVCDFMRCRLVDADGPIARL 657  
 DB 541 CCKKNDPSTCASTSVQMSRHFSGRTITLQPSGPCNDFGVCDFMRCRLVDADGPIARL 600  
 QY 658 KKAIFSPELYENIAEMIVAHMVAVLLMGIALIMLAGFIKICSVHTSPSSNFKLPPPKLP 717  
 DB 601 KKAIFSPELYENIAEMIVAHMVAVLLMGIALIMLAGFIKICSVHTSPSSNFKLPPPKLP 660  
 QY 718 GTLKRPRRPOPLOPOROPRPSYOMGHMR 748  
 DB 661 GTLKRPRRPOPLOPOROPRPSYOMGHMR 691

RESULT 5  
 ID 010743 PRELIMINARY; PRT: 544 AA.  
 AC 010743:  
 DT 01-NOV-1996 (Triblrel. 01, Created)  
 DT 01-NOV-1996 (Triblrel. 01, Last sequence update)  
 DT 01-JUN-2001 (Triblrel. 17, Last annotation update)  
 DE DISINTEGRIN-METALLOPROTEASE PRECURSOR (EC 3.4.24.-) (MYELIN-ASSOCIATED METALLOPROTEINASE) (MADM) (FRAGMENT).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NX NCBI\_TaxID=10116;

RP [1]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN-SPRAGUE-DAMLEY; TISSUE-BRAIN;  
 RA MEDLINE=96276398; PubMed-8694785;  
 RA Howard L., Mitchell S., Lu X., Griffiths S., Glynn P.;  
 RT "Molecular cloning of MADM: a catalytically active mammalian  
 RT disintegrin-metalloprotease expressed in various cell types."  
 RL Biochem. J. 317:45-50(1996).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B (ZINC  
 CC METALLOPROTEASE); ALSO KNOWN AS THE REPOLYSIN SUBFAMILY.  
 CC -1- SIMILARITY: HIGH, IN THE MIDDLE REGION, TO DISINTEGRINS.  
 DR EMBL: Z48444; CA88359.1; -  
 DR HSP: P18619; IFLV.  
 DR MEROPS: M12.210; -  
 DR InterPro: IPR001762; Disintegrin.  
 DR InterPro: IPR001590; Repolysin.  
 DR InterPro: IPR000130; ZnMTpeptidse.  
 DR Pfam: PF00200; disintegrin; 1.  
 DR Pfam: PF01421; Repolysin; 1.  
 DR PRINTS: PR00289; DISINTEGRIN.  
 DR SMART: SM00050; DISIN. 1.  
 DR PROSITE: PS0215; ADAM\_MERPO: 1.  
 DR PROSITE: PS0214; DISINTEGRIN 2; 1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
 KM Integrin; Hyaluronase; Metalloprotease; Transmembrane; Zinc; Signal;  
 KM Glycoprotein.  
 FT NON\_TER 1  
 FT SIGNAL <1 9  
 FT CHAIN 10 241  
 FT CHAIN 242 346  
 FT DOMAIN 10 468  
 FT TRANSMEM 469 492  
 FT DOMAIN 493 544  
 FT ACT SITE 180 180  
 FT METAL 179 179  
 FT METAL 183 183  
 FT METAL 189 189  
 FT CARBOHYD 63 63  
 FT CARBOHYD 74 74  
 FT CARBOHYD 235 235  
 FT CARBOHYD 347 347  
 SQ SEQUENCE 544 AA; 60444 MW; F75E08D6C88A7D0 CRC64;

Query Match 71.4%; Score 2920; DB 11; Length 544;  
 Best Local Similarity 96.9%; Pred. No. 4.7e-231;  
 Matches 527; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 205 GPELLRKRKRNSAEKNTCOLYIQDHLFFKYGTREAVIAQISSHVAIDITYQTDFSG 264  
 DB 1 GPELLRKRKRITLPERNTCOLYIQDHLFFKSYGTREAVIAQISSHVAIDITYQTDFSG 60  
 QY 265 IRTNSFWKRIKRIINTTADKDPNPPRPNTGVEKFLNESEONHDDYCLAYVETDRED 324  
 DB 61 IRTNSFWKRIKRIINTTADKDPNPPRPNTGVEKFLNESEONHDDYCLAYVETDRED 120  
 QY 325 DGVIGLAWGAPSGSGGICEKSKLYSDGKKSLMTGIIYQVNGSHVPRKVSHTFAHE 384  
 DB 121 DGVIGLAWGAPSGSGGICEKSKLYSDGKKSLMTGIIYQVNGSHVPRKVSHTFAHE 180  
 QY 385 VGHNFSGPHDSGTECTPGESKNIQKENGNTIMVARATSGKLNKFNFSCLISINISQV 444  
 DB 181 VGHNFSGPHDSGTECTPGESKNIQKENGNTIMVARATSGKLNKFNFSCLISINISQV 240  
 QY 445 EKKRNNCFVESGQPIGANGVGECECDGYSQCKDCCPDANQPSGRCKLPKQKCS 504  
 DB 241 EKKRNNCFVESGQPIGANGVGECECDGYSQCKDCCPDANQPSGRCKLPKQKCS 300  
 QY 505 PSQGPCTAQAQAFKSKSEKCRDSDSCAREGICNGFTALCPASDPKPNFTDCNRRHTQV 564  
 DB 301 PSQGPCTAQAQAFKSKSEKCRDSDSCAREGICNGFTALCPASDPKPNFTDCNRRHTQV 360

Db 421 ATSGDKLNNNKFSLSIRNISOVLEKRRNNCFVESGQPIGNGMVEGEECDGYSDDCK 480

QY 481 DECCFDANOPGEGKCKLPGKOCSPSGPCCCTACAFKSKSEKCRDSDCAREGICNGFT 540

Db 481 DECCFDANOPGEGKCKLPGKOCSPSGPCCCTACAFKSKSEKCRDSDCAREGICNGFT 540

QY 541 ALCPASDPKPNFTDCNRHTQVCINGOCAGSICEKHGLEBECTCASSDCKDKELCHVCCMK 600

Db 541 ALCPASDPKPNFTDCNRHTQVCINGOCAGSICEKHGLEBECTCASSDCKDKELCHVCCMK 600

QY 601 KMDPSTCAGSVOGSRHFSGRITTLQPGSPCNDPRGCDVFMRCGLVDADGPLARLAKKA 660

Db 601 KMDPSTCAGSVOGSRHFSGRITTLQPGSPCNDPRGCDVFMRCGLVDADGPLARLAKKA 660

QY 661 TSPPELYENIAEWIYAHMVAVLMLGALIMLAGFKICSVTPSSNPKLPKPLPGTL 720

Db 661 TSPPELYENIAEWIYAHMVAVLMLGALIMLAGFKICSVTPSSNPKLPKPLPGTL 720

QY 721 KRRRPPPTIOQPOROPRESYOMGHMR 748

Db 721 KRRRPPPTIOQPOROPRESYOMGHMR 748

RESULT 3

ID 035598 PRELIMINARY; PRT; 749 AA.

AC 035598;

DT 01-JAN-1998 (TREMBlrel. 05, Created)

DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE KUZANIAN.

GN ADAM10 OR KUZ.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97386452; PubMed=9244301;

RA Pan D., Rubin G.M.,

RT "Kuzbanian controls proteolytic processing of Notch and mediates lateral inhibition during Drosophila and vertebrate neurogenesis."

RL Cell 90:271-280(1997).

DR EMBL: AF011379; AAC53303.1; -

DR HSSP: P18619; 1FVL.

DR MEROPS: M12.211; -

DR MGD: MGI:109548; Adam10.

DR InterPro: IPR001762; Disintegrin.

DR InterPro: IPR001590; Reptolysin.

DR InterPro: IPR00130; Zn\_Mtpeptidase.

DR Pfam: PF00200; disintegrin\_1.

DR Pfam: PF01421; Reptolysin\_1.

DR SMART: SM00050; DISIN: 1.

DR PROSITE: PS50215; ADAM\_MEROPS: 1.

DR PROSITE: PS50214; DISINTEGRIN\_2: 1.

DR PROSITE: PS00142; ZINC\_PROTEASE: UNKNOWN.1.

SQ SEQUENCE 749 AA; 83966 MW; 06CEC3EB2CFAF94 CRC64;

Query Match 93.0%; Score 3804.5; DB 11; Length 749;

Best Local Similarity 93.1%; Pred. No. 0;

Matches 697; Conservative 18; Mismatches 33; Indels 1; Gaps 1;

QY 1 NVILRLVLTLLSMAGCGCGNPLNRYIRHYEGLSYNNVSLQKHQRKRAVSHEDFL 60

Db 1 NVILRLVLTLLSMAGCGCGNPLNRYIRHYEGLSYNNVSLQKHQRKRAVSHEDFL 60

QY 61 RUDFNAHGHNFNLRMKRDTSLSDEFKVEYSNKVLDYDTSHTYTGHIYEGESLMLGLL 120

Db 61 RUDFNAHGHNFNLRMKRDTSLSDEFKVEYSNKVLDYDTSHTYTGHIYEGESLMLGLL 120

QY 61 LDFEFAHGHQFNLRMKRDTSLSDEFKVEYSNKVLDYDTSHTYTGHIYEGESLMLGLL 120

Db 61 LDFEFAHGHQFNLRMKRDTSLSDEFKVEYSNKVLDYDTSHTYTGHIYEGESLMLGLL 120

QY 121 MEDLQSSSLVVAHFMFPAERYIKDRILPHFSVHYEDDINPFRHYGSGGCAHSVFE 180

Db 121 MEDLQSSSLVVAHFMFPAERYIKDRILPHFSVHYEDDINPFRHYGSGGCAHSVFE 180

Db 121 DGRFEGFIKTRGGFTYTEPARYIKDRILPHFSVHYEDDINPFRHYGSGGCAHSVFE 180

QY 181 RMRYOMTGVVEEYQIQDEHAA-NGPELLRRKRFRNSAEKNTQCLYTQDHLFFKYGYTR 239

Db 181 RMRYOMTGVVEEYQIQDEHAA-NGPELLRRKRFRNSAEKNTQCLYTQDHLFFKYGYTR 239

QY 240 EAVIAQISSHVKALDITYQTTDFSGIRNISEFWKRIKRIINTADEKDPINPRFRNIGYER 299

Db 240 EAVIAQISSHVKALDITYQTTDFSGIRNISEFWKRIKRIINTADEKDPINPRFRNIGYER 299

QY 300 FLELNSQNDHDDYCLAVFTDRDFDGVGLAMVAGPAGSSGAGICEKSKLYSDGKKKSLN 359

Db 301 FLELNSQNDHDDYCLAVFTDRDFDGVGLAMVAGPAGSSGAGICEKSKLYSDGKKKSLN 359

QY 360 TGIITVYONGSHVPPKSHITTEFAEHGHNFGSPHDSGIBCPGSKNLGCKENQNTYMTA 419

Db 361 TGIITVYONGSHVPPKSHITTEFAEHGHNFGSPHDSGIBCPGSKNLGCKENQNTYMTA 420

QY 420 RATSGDKLNNNKFSLSIRNISOVLEKRRNNCFVESGQPIGNGMVEGEECDGYSDDCK 479

Db 421 RATSGDKLNNNKFSLSIRNISOVLEKRRNNCFVESGQPIGNGMVEGEECDGYSDDCK 480

QY 480 KDECFTDANOPGEGKCKLPGKOCSPSGPCCCTACAFKSKSEKCRDSDCAREGICNGFT 539

Db 481 KDECFTDANOPGEGKCKLPGKOCSPSGPCCCTACAFKSKSEKCRDSDCAREGICNGFT 540

QY 540 TALCPASDPKPNFTDCNRHTQVCINGOCAGSICEKHGLEBECTCASSDCKDKELCHVCCMK 599

Db 541 TALCPASDPKPNFTDCNRHTQVCINGOCAGSICEKHGLEBECTCASSDCKDKELCHVCCMK 600

QY 600 KMDPSTCAGSVOGSRHFSGRITTLQPGSPCNDPRGCDVFMRCGLVDADGPLARLAKKA 659

Db 601 KMDPSTCAGSVOGSRHFSGRITTLQPGSPCNDPRGCDVFMRCGLVDADGPLARLAKKA 660

QY 660 AIFSPPELYENIAEWIYAHMVAVLMLGALIMLAGFKICSVTPSSNPKLPKPLPGT 719

Db 661 AIFSPPELYENIAEWIYAHMVAVLMLGALIMLAGFKICSVTPSSNPKLPKPLPGT 720

QY 720 LKRRPPPTIOQPOROPRESYOMGHMR 748

Db 721 LKRRPPPTIOQPOROPRESYOMGHMR 749

RESULT 4

ID 010742 PRELIMINARY; PRT; 691 AA.

AC 010742; Q92650;

DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE DISINTEGRIN-METALLOPROTEASE MADM (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96276396; PubMed=8694785;

RA Howard L., Lu X., Mitchell S., Griffiths S., Glynn P.,

RT "Molecular cloning of MADM: a catalytically active mammalian disintegrin-metalloprotease expressed in various cell types."

RL Biochem. J. 317:45-50(1996).

DR EMBL: Z48579; CA88463.1; -

DR HSSP: P18619; 1FVL.

DR MEROPS: M12.210; -

DR InterPro: IPR001762; Disintegrin.

DR InterPro: IPR001590; Reptolysin.

DR InterPro: IPR00130; Zn\_Mtpeptidase.

DR Pfam: PF00200; disintegrin\_1.

DR Pfam: PF01421; Reptolysin\_1.

DR PRINTS: PRO0289; DISINTEGRIN.

DR SMART: SM00050; DISIN: 1.

DR PROSITE: PS50215; ADAM\_MEROPS: 1.



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OY 614 QMSRHSRRTITLPGSPCNDPFGYCDVFMRCRLVADGDLARLKAIFSPPELYENIAEW 673
DB 846 ADKVIYQKGISLIDPGSCDNFQGYCDVFLKRAVDADPLRLKLNRLNLRKTLQIYAEW 905
OY 674 IVAHMAVLLMGIALIMLMAGFIKCSVHPSSNPKLPGLPTLKRPRRPPDIOQPO 733
DB 906 IVDNMYLVYLVAGVFIYVWGSFICCAVHPSSNPKRRARRRISFTL--RAPMNTLRMO 963
OY 734 R---OR-----PRESYONGHMR 748
DB 964 RHPNORGAGPSRIPPAHQAHSR 988

RESULT 7
OY Q9NKF9 PRELIMINARY; PRT: 1236 AA.
AC Q9NKF9;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE KUZ PROTEIN.
GN KUZ OR BG:DS07660.3 OR CG7147.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Y, CN BW SP;
RX MEDLINE=99403001; PubMed=10471707;
RA Ashburner M., Mista S., Roote J., Lewis S.E., Blazej R., Davis T.,
RA Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshireli A.,
RA Palazzolo M., Reese M.G., Spreading A., Tsang G., Wan K., Whiteclaw K.,
RA Celisner S., Rubin G.M.;
RT "An exploitation of the sequence of a 2.9-Mb region of the genome of
RT Drosophila melanogaster: the Adh region.";
RL Genetics 153:179-219(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Y, CN BW SP;
RA Celisner S.E., Agbayan A., Arcalona T.T., Baxter E., Blazej R.G.,
RA Buehner C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
RA Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
RA Houston K.A., Hummasti S.R., Karia K., Kearney L., Kim E., Lee B.,
RA Lewis S., Li P., Lomocan M.A., Mazda P., Moshireli A.R., Moshireli M.,
RA Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequelira A.,
RA Sethi H., Snir E., Svitskas R.R., Wan K.H., Weinburg T., Zhang R.,
RA Zieran L.L., Rubin G.M.;
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AE003407; AAF4800.1; -.
DR Flybase: FB00015954; kuz.
DR InterPro: IPR001762; Disintegrin.
DR InterPro: IPR001590; Reptolysin.
DR InterPro: IPR001030; Zn_MTPetase.
DR SMART: SM00050; DISIN. 1.
DR PROSITE: PS50215; ADAM_MEPRO; 1.
DR PROSITE: PS50214; DISINTEGRIN_2; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
SO SEQUENCE 1236 AA; 136343 MW; 40461AC17040C9AD CRC64;

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Query Match 35.5%; Score 1451; DB 5; Length 1236;  
 Best Local Similarity 34.3%; Pred. No. 4,2e-110;  
 Matches 331; Conservative 124; Mismatches 256; Indels 254; Gaps 23;

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DB 94 KLDFYDSKGFIDVSTOHIEYGEVIGDRNSYVGSIHNGVFGKILTERDAYVEHAKHYF 153
OY 120 ----- 119
DB 154 PTKNTATTPPSTSTSSATTAATKSTQTPRLAKNSSTTAVNSKTEFNFKIAESTYTS 213
OY 120 --LMEDLKDSRLVVAHFMPEPAERYTKDR-----TLPHSVTY--HEDDINTPHY 167
DB 214 QQLPEYTESSSSTTT--PPPTTEFEDEKERNADELDPSHTIYESHVEFAYENVE 270
OY 168 GPQGGCA-DHSVEFRMRKQTMGVLEVYD-----IPEBHANAGP-- 206
DB 271 GHVAGCGITDEVQSMMENIIONSAVELPEPMSKDYQLHRKQLHKSAPOOQOQPHPPK 330
OY 207 -----ELTKRKKTNSA 217
DB 331 YISGDEDFKYPHQKTKKEANFAGAFYDPSITGRGLSSANVADHMLQVHERVARRADNGA 390
OY 218 -----EKNTQQLYQTDHLFEYTY-----GTREAVIAQ 245
DB 391 GDRSGSGSGRGREDNKNKTCSTLYQTPDLIMHIREGIDHDKRKYEVDEKTRREITSL 450
OY 246 ISSHVKADITYQTFDFSG---IRNISFVKRIRINTA---DEKPTNPFPPNIGVE 298
DB 451 IAHVTVAVNTYRNTKFDGRTERRNIRFEVQRIKIDDSACRNSYNGPHNAFCNEMHVS 510
OY 299 KFLINSEQNHDDYCLAYVPTDRPDYGLIAMGAPSGSGGICRKSILYD----- 352
DB 511 NFLNHSLEDHSDPCLAYVFTYDFGTGLIAMVASASGSGICRKYTYVETWGGQY 570
OY 353 -GRRKSINTGITYVQYSHVPPKYSHIFFAHEVGHNSPHDGTCTGTGESKNLGORE 411
DB 571 QSTRKSLNTGITEFVYVNSRVPKVSQTLHAIEIGHNCSPHDYPOECRFGGL----- 623
OY 412 NGNTIMARTSGDKLNKFKSLICSTRINSOYLE---KRNKCFVSSGQPIGNGNVED 467
DB 624 NGNTIMFASATSGDRPNKSFSPCSIRNISNLDVVGNTNRDCKFKASBGAFCGNKIVS 683
OY 468 GEEDCGYS--DOCKDECCF-----DANQPEGRKCKLPGKCSPSDQPCCTA--QCAF 517
DB 684 GEEDCGFNEEBCCKDCYPRILISEYDQSLNSAKCTRRAKTQCSPOGPCCLNSGTF 743
OY 518 --KSKSEKCDSDDCAREGICNGFALCPASPKRNTFDCRNRHNOVONOCAGSICERY 575
DB 744 VPTSHOKCKELETCSSMSTCMTGTAECPEPHRDKTMCNNGTALCIRREGSGSPCLLM 803
OY 576 GLEBC--TCASSDGKDKELCHAYCCKMKMDPSTCASIGSVYMSHNFSGRTITLQPSPCN 633
DB 804 NMTKCFUTSTTLPHVASKRKICDLACODGNDYTCRSTSEFADKYNIGKGISLDPSPCD 863
OY 634 DFGYCDVFMRCRLVADGDLARLKAIFSPPELYENIAEWIVAHMAVLLMGIALIMLM 693
DB 864 NFGYCVFLKRAVDADPLRLKLNRLNLRKTLQIYAEWIVYLVLMAGVFIYVWG 923
OY 694 GFITCSVHPSSNPKLPPLPKLPGLPTLKRPRRPPDIOQPO--OR-----PRESYON 743
DB 924 SFIKCAVHPSSNPKRRARRRISFTL--RAPMNTLRMORHPNORGAGPSRIPPAHQA 981
OY 744 GHMR 748
DB 982 QHYSR 986

RESULT 8
OY 094902 PRELIMINARY; PRT: 1239 AA.
AC 094902;
DT 01-FEB-1997 (TREMblrel. 02, Created)
DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE KUZBANIAN.
GN KUZ OR BG:DS07660.3 OR CG7147.
OS Drosophila melanogaster (Fruit fly).

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Db 85 DDLSEHEDMSVDGADYADIRPSHFLEYGLKDDPNASHGSGVDFGEHIGTG----- 139
Qy 123 DLKSSRLVAVHFEPAERYIK--DRTLPFSVLYHEDDIY-----PKHYPOG 171
Db 140 ---EGRR---YSIDKAAKYFERDRPRQYHSIITYRDEIYHNRKWKRYKRAENLSDQM 191
Qy 172 GCADHVSFERKRYOMTGV---EYQIQOEHAANGPELLKRTKNTNAEN-----T 221
Db 192 GCGFSS---KRR-EMTDVONSGESDFTNTMTMG-----RSKANTLRDHDGLYVRT 243
Qy 222 COLYIOTDHEFKY-----YGTREAVIAQISSHVKAIDITYOTTFDSGIRNISFM 271
Db 244 CSLWQADHKIKYEHIRKKEGNNDPIRTREIYSLFYNHKAIVNEIESTNGIKGJHFV 303
Qy 272 VKRIRIN--TAD-----EKDPTNPRFRPNIGVEKLELMSBQNDHDDCYLAVFDRPDD 325
Db 304 IORSTIYTPDCDGRKAKTSDNPCEBENDVSNFNLMSQSNHAPFLAVALFRPFGV 363
Qy 336 GVLGLAWGAPS-GSSGIGCKSKLYSDGR-----KSLNTGIIYQYNGSHVPRVSHIT 380
Db 364 GTGLAWWASQFMTAGICQVHORYNESRGWVYSLTGTIVLVNGBRVPARYSOLT 423
Qy 381 FAHEVGHFSGSDHSGTECPGSESKNLGQKENGNYIMVARASGDKLNNKFSICIRNI 440
Db 424 LAHEIGHNFGSPHFPAPDCOPG-----LPDGNFIMFASATSGDKPNNGKFSYKNI 476
Qy 441 SQVL-----EKRRN-----NCFVESGPICGNGVEEGECDCGYS---DQ 478
Db 477 SAVILAVLKSMPVDPTRNAPSVGIGRKNCFOEETSAFCNOIYEEGDCDCGFSQADCDQ 536
Qy 479 CKDECCFANPREG---KCKLKGKCSGSPSGPCCPTAQ--CAFKSEK--CRDSDCA 531
Db 537 MDCKCV-PHARANGNGRPGCKRKPAGCSPSGICVQCNPDTSLSGKNEKIKQSEBSC 595
Qy 532 RBGICNGFTALCPASDPKPNFTCCNRHTOYCINGCAGSICGKYIELECTCASSDGDOK 591
Db 596 NLQCTDGNNAOCPPVSPKHGICQDOSTKVCSSGCGNSVCMFLFEDCFL--TEGAD- 652
Qy 592 ELCHVCKKKMDPSTCASTGVSOMSRHFSGRT-----TLPGSPCNDGFRGVC 639
Db 653 ELCLACAK---DGKC--TSSVHLPEFSANRTWFLQNMKDKPGILLRPSGPNKNGYGC 707
Qy 640 DYFMRCLYVDADGFLAKLKAISPELEYEMIAHYAMVAVLGLMGLMAGFKIC 699
Db 708 DIFRRCRSVDANGPLARKLNLFNKRTIETLTQWADNMWVGVLVLMLEFVCC 767
Qy 700 SVHTPSSNPKLPKPKPL-----PGLTKRR-----PPQIQOPQ 733
Db 768 AVHTPSTNPKPRALNTYQTLTRPGTLIRQHQRHRAAGSVRPGAPR 818

RESULT 10
QyVA12 PREDIMINARY; PRT; 1537 AA.
ID QyVA12;
AC QyVA12;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CG1964 PROTEIN.
GN CG1964.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX ADAMS M.D., CELINKER S.E., HOLT R.A., EVANS C.A., GOCAYNE J.D.,
RA AMANATIDES P.G., SCHERER S.E., LI P.W., HOSKINS R., GALLE R.F.,
RA GEORGE R.A., LEWIS S.E., RICHARDS S., ASHBURNER M., HENDERSON S.N.,

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RA SUTTON G.G., WORTMAN J.R., YANDELL M.D., ZHANG Q., CHEN L.X.,
RA BRANDON R.C., ROGERS Y.-H.C., BLAZEJ R.G., CHAMPE M., PFEIFFER B.D.,
RA WAN K.H., DOYLE C., BAXTER E.G., HELT J.G., NELSON C.R., MILLER G.L.G.,
RA BULL J.F., ABAYANAI A., AN H.-J., ANDREWS-PHILMOUCH C., BALDWIN D.,
RA BALLEW R.M., BASU A., BAXENDALE J., BAYRAKTAROGULU L., BEASLEY E.M.,
RA BEESON K.Y., BENOS P.V., BERMAN B.P., BHANDARI D., BOLSHAKOV S.,
RA BORKOVA D., BOTCHAN M.R., HOUCK J., BROKSTEIN P., BOTTIER P.,
RA BURTIS K.C., BUSAN D.A., BUTLER H., CADIEUX E., GENTER A., CHANDRA I.,
RA CHERRY J.M., CAWLEY S., DAHLKE C., DAVENPORT L.B., DAVIES P.,
RA DE PABLOS B., DELCHER A., DENG Z., MAYS A.D., DEW I., DIELZ S.M.,
RA DODSON K., DONG L.E., DOWNES M., DUGAN-ROCHA S., DUNKOV B.C., DUNN P.,
RA DUBILIN K.J., EVANGELISTA C.C., FERRAZ C., FERLIERA S., FLEISCHMANN W.,
RA FOSTER C., GABRIELIAN A.E., GARG N.S., GELBART W.M., GLASSER K.,
RA FLODEK A., GONG F., GORRELL J.H., GU Z., GUAN P., HARRIS M.,
RA HARRIS N.L., HARVEY D., HELMAN T.J., HERNANDEZ J.R., HOUCK J.,
RA HOSTIN D., HOUSTON K.A., HOWLAND T.J., WEI M.-H., IDEGAM C.,
RA JARALI M., KALUSH F., KARPEN G.H., KE Z., KENNISON J.A., KETCHUM K.A.,
RA KIMMEL B.E., KODIRA C.D., KRAFT C., KRAVITZ S., KULP D., LAI Z.,
RA LASKO P., LEI Y., LEVITSKY A.A., LI J., LI Z., LIANG Y., LIN X.,
RA LIU X., MATTEL B., MCINTOSH T.C., MCLEOD M.P., MCPHERSON D.,
RA MERKULOV G., MILSHINA N.V., MOHARRY C., MORRIS J., MOSHREFI A.,
RA MOUNT S.M., MOY M., MURPHY B., MURPHY L., MUZY D.M., NELSON D.L.,
RA NELSON D.R., NELSON K.A., NIXON K., NUSKERN D.R., PACLEB J.M.,
RA PALAZZOLO M., PITTMAN G.S., PAN S., POLLARD J., PURI V., REESE M.G.,
RA REINERT K., REMINGTON K., SAUNDERS R.D.C., SCHUELER F., SHEN H.,
RA SHUE B.C., SIDEN-KIAMOS I., SIMPSON M., SKUPSKI M.P., SMITH T.,
RA SPIER E., SPEDLING A.C., STAPLETON M., STONG R., SUN E.,
RA SVIRSKAS R., TECTOR C., TURNER R., VENTER E., WANG A.H., WANG X.,
RA WANG Z.-Y., MASSARAME D.A., WEINSTOCK G.M., WEISENBACH J.,
RA WILLIAMS S.M., WOODDAR T., WORLEY K.C., WU D., YANG S., YAO Q.A.,
RA YE J., YEH R.-P., ZAVETI J.S., ZHAN M., ZHANG G., ZHAO Q., ZHENG L.,
RA ZHANG X.H., ZHONG F.N., ZHONG W., ZHOU X., ZHU S., ZHU X., SMITH H.O.,
RA GIBBS R.A., MYERS E.M., RUBIN G.M., VENTER J.C.;
RA "the genome sequence of Drosophila melanogaster.";
RL Science 287:2195-2195(2000).
CC -1- STIMILARITY: TO NEUTRAL ZINC METALLOPEPTIDASES, ZINC-BINDING REGION
CC DOMAIN.
DR EMBL; AE003770; AAF56926.1; -.
DR HSSP; P18619; 1FVL.
DR FlyBase; FBgn0039688; CG1964.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR001590; Reprolysin.
DR InterPro; IPR00130; zn_mpeptidse.
DR Pfam; PF01421; Reprolysin; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS50215; ADAM_MEPRO; 2.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR HydroLase; Metalloprotease; Zinc.
SQ SEQUENCE 1537 AA; 168796 MW; 46A52344AE72617 CRC64;

Query Match 32.9%; Score 1345.5; DB 5; Length 1537;
Best Local Similarity 33.0%; Pred. No. 2,56-101;
Matches 321; Conservative 108; Mismatches 258; Indels 285; Gaps 27;

Qy 4 LRVILLISMAAG-----MGGYGNPLNKYIRYEGLSYN-----VDSLHOK 45
Db 10 LQVLEFLMLLPEELIALIPPLKIPG-YTHRLTPYIKIMEANRDQVLAQVRLLEDA 68
Qy 46 HQRAKRVSHEDQFL---RLDFHAGHFNILRMKRTD-SLFSDEKVEVTSNKVLDYDTS 100
Db 69 RFRKREKREYTSASGLNHTIRLNFNSAIDRFRVLVLRQSHSVFADVDIEVTLQPIDYVS 128
Qy 101 HIYGHYIGEGLSLAGLMLMEDLKDS-RLVAVHFEPAERYIKD-RLFPHSYATYE 158
Db 129 RITYGSLEDEAHVQALITSDNLDTETFGAEHYIYEPNHRSSQGLASSGVHSIYVKI 188
Qy 159 DDINYPIKHYPOGG-----CADHSV----- 178
Db 189 SDVNMKQKQFTGGLSANPAKTHCKSEKIRKKRWLPEELAMSDAPATYNNRNPPLDL 248
Qy 179 -----FERMKRYOMTG----- 189

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DR InterPro: IPR000130; Zn\_MTPeptide.  
 DR SMART: SM00050; DISIN\_1.  
 DR PROSITE: PS50215; ADAM\_MEPPO; 1.  
 DR PROSITE: PS50214; DISINTEGRIN\_2; 1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
 KW Protease; Metalloprotease.  
 SQ SEQUENCE 686 AA; 77298 MW; 66d58008a207a49 CRC64;

Query Match 11.6%; Score 475; DR 5; Length 686;  
 Best Local Similarity 24.8%; Pred. No. 2e-30;

Matches 179; Conservative 100; Mismatches 259; Indels 184; Gaps 37;

69 RHFMIRMKRPTSLFSDPEKVENKVLDTSTHYTGHIYEGESGLAMGLIMEDLK---125  
 28 RHAFIRPQSRQSVAFHPEFDDEYVDLEPNH-STFH-----ENKVFVF 71  
 126 -DSSRLVAFHPEPAERYTKDRLP-----FHSYIHEDDI-----NYPH 165  
 72 QDGPQIV-----PRDEYIGYRFRAGRAVLTQLEENYVIGSLYFVDDTLHLEPSY 124  
 166 K-----YEPQGCADHSY-----FERMKYQMTGVEEYVQIPEEHANG 205  
 125 QLSDDLPVYGVGFESDLNLDLSAMPVANGVSFRANPFLKH--RAIALPSP-----176  
 206 PELLRKRTSAEKNICQLYIOTDHLFFKYGTREAVIAQ--ISSHKALDIY-----257  
 177 ---RRKVDLVNKRNRCTKLVDVSEYISFGKNTGIVTFVLNMLARVETITPINMD 232  
 258 --QTTDFSG---IRNISFWYKRIINTADEDPNPPRPNI-GVEKFL-ELNSEQNDH 310  
 233 VGRDDSDISGRFRQNMGSFKEIKVLDRPNASD-SHNSYSRIMVEVLEEFAPAGSK 291  
 311 DYCLAVYFTDRDD-GVGLAWYGAAP--SGSSGICRKSRLYSGKKSLNGLIT--V 365  
 292 DFCVLHVTARTREAVATLGLAVSYKKWDETAGGICSKOETF-NGRAVINYLLSTFA 350  
 366 QNYGSHVP--PKVSHITFAHEVGHNFSPHD-----SGTECPGSEKNLQKENGNY 415  
 351 NSBSTPTPLTKKEIDIVYSHHYGHANGATHDPTIDSDPDVEECSPND-----QNGCKY 404  
 416 IMYKATSGDKLNNKPSLCSIRNISQVLEKRRNCFVESGQPIGCGNMGVQEGECG 475  
 405 LMSQYAGKYDANNVLEFPCSRKLIQVILIGWESCFQEMHSTFCGNQIYVDEGECNGV 464  
 476 SDQCKDECCDANQPEGRCKLKPQKQSPSGPCCYACAFKSKSEKC--RDDSICARE 533  
 465 DTDFNEFNC-----DKFCRLAVGAKSPMLHICCTPTCOFHNSHTVCLFGDSLCKAD 517  
 534 GICNGFTALCPASDPKPNFTDCNRHTQVINCAGASICEK--VGELECTCASSDGKDK 591  
 518 AVCNQFGECECSAPVADQGECEGSE-CLNGVCL-PRCEKMSIGKSKSCIC-----EDL 569  
 552 EL-CHVCCMKMKMDSCTCAGSYQVMSRHSFSGRTITLQSPQPCNDPRGCDVFRCLYDA 650  
 570 ELSCRLCC--RDYNGTCAPVPG-----HYVLRGVRS--KQSC-----604  
 651 DGPIRLAKKALFSELYEN-----IAEWIAHMAVAILGLIALILMAGFI 696  
 605 -----RDRKCV--NEVVDNVRNFIITPOTGTGVLEFIKTH--LVYALIIIFTLIFGIY 655  
 697 KI 698  
 656 KI 657

RESULT 13

OPPVK7 PRELIMINARY; PRT: 600 AA.

AC 09PVK7;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, last annotation update)

DE COBRIN PRECURSOR.  
 OS Naja naja (Indian cobra).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Elapidae; Elapinae; Naja.  
 OX NCBI\_TaxID=35670;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=KAOUTHIA; TISSUE=VENOM GLAND;  
 RA Bambaï B., Bredemort R., Vogel C.-W.;  
 RL Submitted (Mar-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF063190; AAF00693.1; -.

DR HSSP: P17494; 1KST.

DR InterPro: IPR001762; Disintegrin.

DR InterPro: IPR002870; Pep\_M12B\_propep.

DR InterPro: IPR001590; Reprolysin.

DR InterPro: IPR000130; Zn\_MTPeptide.

DR Pfam: PF00200; disintegrin\_1.

DR Pfam: PF01562; Pep\_M12B\_propep; 1.

DR Pfam: PF01421; Reprolysin; 1.

DR PRINTS: PR00289; DISINTEGRIN.

DR ProDom: PD000664; DISINTEGRIN.

DR SMART: SM00050; DISIN.

DR PROSITE: PS50215; ADAM\_MEPPO; 1.

DR PROSITE: PS50214; DISINTEGRIN\_2; 1.

DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.

KW Signal.

FT SIGNAL.

FT CHAIN.

EQ SEQUENCE 600 AA; 67661 MW; C7C0D45BEC694290 CRC64;

Query Match 10.0%; Score 409.5; DR 13; Length 600;  
 Best Local Similarity 24.1%; Pred. No. 4e-25;

Matches 158; Conservative 90; Mismatches 234; Indels 173; Gaps 30;

47 QRAKRAVSHEDQFLRLDFHAGRHFNLMKADTSLFSDER-----KYETSKYLD 96  
 36 QNPQPEKTEED-MQYEFQVNGEPVLLERNNKLFSDDYETHTVAPDGEITSPVOD 94  
 97 YDTSHTYGHYEGESGLAMGLIMEDLKSSRLVNAHFEPAERYIKDRLTFHSVLY 156  
 95 H--CYHGFQVQEAQSSAV-ISACDGLKGFKLQGEIYFLEP-----LKISDEAAIY- 145  
 157 HEDDINPRAHYGQSGCADHSYFERMKRYQNTGYEVT-----QIPEEHAANGPELLRK 211  
 146 -----KDENVEEDETPKICGVTDVTSWSEDEPKTSLITNTP--Q 185  
 212 KRTNSAEKNTCOLYIOTDHLFFKYGTREAVI-AQISSHAKAIDITYOTTDFSGIRNISI 270  
 186 DRYLQAEK-YIEYVAVVONIMRHKKRQVLYIKKRYEMINTMIMYIRLNF-----HIAL 240  
 271 MKKRI-----KINTADEDPNPPRPFNIGVEKFLLENSQNHNDYCLAVYTDKRPDD 325  
 241 IGLIWSNINEIIVQSDVAVATLDL--GEEMEKLLPKRRDN--AQLLTGIDFNG 292  
 326 GVGLAWGAPSGSSSGICEKSLYSDGKKSLNTGITTYQNYGSHVPPKVSHTFAHEV 385  
 293 TVPGLAYIGS-----ICNP-----KTSAAVYQDQSKF--RMVAITWAMEM 331  
 386 GHNFGPSHDSGTCTGTGSEKSLNGQKENGNYIMYARAISGDKLNNKFSLSICIRNISQYLE 445  
 332 GHNLGMNHDKGF-CTCGFNK-----CVMSTRRTK---PAYQSSCSVNEHQRYLL 377  
 446 KRRNCFVES-----GQPIGCGNMGVQEGECGYSQCKDECCFDANQPEGRCKKLK 498  
 378 RDRPQCLINKPLSTDIVSPICGNFVEVGECCGSPADQGSAC-----NATCKQLQ 431  
 499 PKQKQSPGSPCTACAFKSKSEKCR--DSDSCAREGICGNFALCPASDPKPNFTDCNR 557  
 432 HEAQCSSEB--CCCKCKFKAGAGACRAKDDCLPELCTGQSECPCTDVFDKNGLPC-Q 487  
 558 HTQVCIINGOC-----AGSICEKYGLEECTCASSD 586

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DB 488 NNGCYKNGKMTNOCIALRGPYKVSNDSCFTLNTQRCGCLCRMEYV-RHPCADND 546
QY 587 GKDKELCHV-----CCMKKMDSTASGVSQVSNHHSGRITTTQPSPCND 634
DB 547 VKGRLEFCKRSMICNCSISPRDP-----SYGMV-----EPQTKGD 584

RESULT 14
ID 077633 PRELIMINARY: PRT: 75 AA.
AC 077633:
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE DISINTEGRIN-METALLOPROTEINASE PRECURSOR (FRAGMENT).
GN AAM-10.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Flannery C.R., Little C.B., Caterson B., Hughes C.E.;
RT "Expression of articular cartilage metalloproteinases by chondrocytes
RT in fresh tissue and explant, monolayer and agarose cultures.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF069645; AAC23529.1; -
DR MEROPS: M12.210; -
DR InterPro: IPR001590; Reprolysin.
DR PROSITE: PS50215; ADAM_MERPRO; 1.
KW Integrin.
FT NON_TER 1 1
FT NON_TER 75 75
SQ SEQUENCE 75 AA: 8224 MW: C03H70C90I333557 CRC64;

Query Match 9.98; Score 406; DB 6; Length 75;
Best Local Similarity 100.0%; Prid. No. 4.6e-26;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 392 PHDSGTECTPGESKNGKENGNGNTMYARATSGDKLNNKFSCISIRINSOYLEKRRNC 451
DB 1 PHDSGTECTPGESKNGKENGNGNTMYARATSGDKLNNKFSLCSIRINSOYLEKRRNC 60
QY 452 FVESGQPTGCGNMGVE 466
DB 61 FVESGQPTGCGNMGVE 75

RESULT 15
ID 061072 PRELIMINARY: PRT: 845 AA.
AC 061072: 060618; 061853;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CELLULAR DISINTEGRIN-RELATED PROTEIN PRECURSOR (MELTRIN GAMMA).
GN ADAM9 OR MLTNG OR MDC9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-LUNG;
RA MEDLINE-96178079; PubMed-8647900;
RA Westkamp G., Kraetzschmar J.R., Reid M., Blobel C.P.;
RT "MDC3, a widely expressed cellular disintegrin containing cytoplasmic
RT SH3-like domains.";
RL J. Cell Biol. 133:717-726(1996).
RN [2]
RP SEQUENCE OF 426-575 FROM N.A.

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RX MEDLINE-96026308; PubMed-7566181;
RA Yagami-Hironaka T., Sato T., Kurisaki T., Kamijo K., Nabeshima Y.,
RA Fujisawa-Schmura A.;
RT "A metalloproteinase-disintegrin participating in myoblast fusion.";
RL Nature 377:652-656(1995).
RN [3]
RP SEQUENCE OF 432-478 FROM N.A.
RX STRAIN-BALB/C;
RX MEDLINE-94195820; PubMed-8146185;
RA Westkamp G., Blobel C.P.;
RT "A family of cellular proteins related to snake venom disintegrins.";
RT Proc. Natl. Acad. Sci. U.S.A. 91:2748-2751(1994).
CC -1- FUNCTION: MAY MEDIATE CELL-CELL OR CELL-MATRIX INTERACTIONS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
DR EMBL: U06145; AAA18424.1; -
DR EMBL: U01765; AAC52446.1; -
DR EMBL: D50412; BAA08913.1; -
DR HSSP: P18619; IEVL.
DR MEROPS: M12.209; -.
DR MGD: MGI:105376; Adam9.
DR InterPro: IPR001762; Disintegrin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR002870; Rep_M12B_propep.
DR InterPro: IPR001590; Reprolysin.
DR InterPro: IPR000130; Zn_MTPeptide.
DR Pfam: PF00200; disintegrin; 1.
DR Pfam: PF01562; Rep_M12B_propep; 1.
DR Pfam: PF01421; Reprolysin; 1.
DR ProDom: PD000664; Disintegrin; 1.
DR SMART: SM00050; DISIN; 1.
DR SMART: SM00181; EGF; 1.
DR PROSITE: PS50215; ADAM_MERPRO; 1.
DR PROSITE: PS50214; DISINTEGRIN_2; 1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Signal; Glycoprotein; Transmembrane; EGF-like domain; zinc;
KW Metal-binding.
FT SIGNAL 1 29
FT CHAIN 30 845
FT DOMAIN 30 698
FT TRANSMEM 699 718
FT DOMAIN 719 845
FT DOMAIN 413 503
FT DOMAIN 505 634
FT DOMAIN 644 698
FT METAL 347 347
FT METAL 347 348
FT ACT_SITE 348 348
FT METAL 351 351
FT METAL 357 357
FT CARBOHYD 144 144
FT CARBOHYD 154 154
FT CARBOHYD 231 231
FT CARBOHYD 231 231
FT CARBOHYD 381 381
FT CARBOHYD 487 487
FT CARBOHYD 636 636
SQ SEQUENCE 845 AA: 92049 MW: 175628B9DA61674 CRC64;

Query Match 9.68; Score 392.5; DB 11; Length 845;
Best Local Similarity 25.3%; Prid. No. 1.6e-23;
Matches 162; Conservative 94; Mismatches 254; Indels 131; Gaps 33;

QY 9 LLLSN--AAGMGG---QVGNPLNKYIRHYEGLSYVNDLSLQKHOKRAKRVSHEDQFLMD 63
DB 12 LRLRLALACGLGAPVLENGRDLEQYVHLS--SYELTTWKLTKREKRLBSSQOISYV 69
QY 64 FIAHRRHNLNKKRKDTSLFSDQFVETSNK---VLVDYF--SHI-YTGHIYGEBSLA- 115
DB 70 IQAQGKHIIHLERNTDLLPNDPFVYVYVDKESGLSDHNPVOSHCHGYGVEGVNSAVA 129
QY 116 -----MGLLIMEDLKDSRLVVAHPMPAPERYIKDRLPFGHSVYIHEDDINYPKYG 168

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Db 130 VSACGJLGLHLEN-----ASFGEPLH-----NSSHFHIFPMDC---HOEP 172
OY 169 POGGCAHVSFERMRKYOMTGVEEVTOIPEEHHANGPELKRKRTNSAEKNTCOLYIOT 228
Db 173 LRCGVSNRDT-----EKEGTGDEEHH-PSVTOLLRRAVLPQTRYVELFIYV 220
OY 229 DHEFFKYGTGE-AVIAQISSHVKAIDTYQTDFSGIRNTSFMWKIRIRINTADEKPT 287
Db 221 DKERIDMGNQOTAVREEMIRLANIYIDSMIT-----MLNIRIYVGLIWT---DRNPT 271
OY 288 NPFRPNIGVEKFELE-----LNSEQNHDDYCLAYFTDRDDEDDGYLGLAWYGAPSGSSGG 342
Db 272 NIGGAGDVLGNFYQWREKFLITRRRHS---AQVLKKGf-GTAGMAFVGT----- 320
OY 343 ICESKXLYSDCKKKSUNT-GITVOMYGSHPKXSHITFAHEVGHNGSPHDSCTECP 401
Db 321 VCSRS--HAGG---INVGQITVETFAIV-----AHELGHNLGMMHDDGRECF 365
OY 402 GESKMLGKENGNYIMYARATSGDKLNNKFSLSIRNTSOYLEKRRNCFE----- 454
Db 366 GAK-----SCIMNSGAS-----GSRNFSCSAEDPEKLTLNKGSCLINIPKPEA 411
OY 455 SGOPICGNGWVEGEEDCGYSDCK-DECCPDANQPEGRKCKLPGKOCSPSOGPCCTA 513
Db 412 YSAPSCGKLVDPEDCDCTAKECEYDPC-----EGSTCKLSFAEC--AYGDCC-K 462
OY 514 OCAFKSKSEKCR-DDSDCAREGICNGFTALCPASDPKPNFTDCNRRHTQVCJNGOCAGSIC 572
Db 463 DCOFLPGGSMCRGKTSECDPVEYCNSSQFCPPDYFIQNGYPCONSKAYCYNG-----MC 517
OY 573 ERYGLEECTCASSDGDCKDELCHVCCMKKMDP-STCASPQS 612
Db 518 QYDQACQVITGSKAKAAPRDCFTFVNSKGDGRNGCGFGSG 558
```

Search completed: April 1, 2002, 15:12:06  
Job time: 688 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 1, 2002, 15:12:06 ; Search time 98.78 seconds  
(Without alignments)  
392.409 Million cell updates/sec

Title: US-09-871-388-6

Sequence: 1 NSQNHDDYCLAAYFTDRDPE.....KPNFTDCNRHTOVCINGVSI 265

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPTREMBL\_17:\*  
1: sp-archaea:\*  
2: sp-bacteria:\*  
3: sp-fungi:\*  
4: sp-human:\*  
5: sp-invertebrate:\*  
6: sp-mammal:\*  
7: sp-mmc:\*  
8: sp-organella:\*  
9: sp-phage:\*  
10: sp-plant:\*  
11: sp-rodent:\*  
12: sp-virus:\*  
13: sp-vertebrate:\*  
14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1472	99.2	691	4	Q10742
2	1472	99.2	748	4	Q14672
3	1466	98.8	544	11	Q10743
4	1463	98.6	749	11	Q35598
5	1449	97.6	748	6	Q10741
6	784	50.8	1537	5	Q9VA12
7	737	49.7	1236	5	Q9NKF9
8	737	49.7	1238	5	Q9VW9
9	737	46.0	1239	5	Q94902
10	683	46.0	922	5	Q46354
11	406	27.4	75	6	Q77633
12	390	26.3	162	13	Q42568
13	366	24.7	686	5	Q94316
14	298.5	20.1	600	13	Q9PYK7
15	283	19.7	620	13	Q42138
16	292.5	19.7	610	13	Q9DGB9
17	291.5	19.6	845	11	Q61072
18	290	19.5	728	4	Q9B211
19	289.5	19.5	609	13	Q90282

20	286.5	19.3	819	4	Q13443	Q13443 homo sapien
21	282.5	19.0	914	13	Q12960	Q12960 xenopus lae
22	282	19.0	610	13	Q9Y120	Q9Y120 agkistrodon
23	280.5	18.9	920	11	Q35674	Q35674 mus musculu
24	280	18.9	609	13	Q9W6M5	Q9W6M5 agkistrodon
25	280	18.9	610	13	Q93523	Q93523 bothrops ja
26	279	18.8	606	13	Q98UP9	Q98UP9 bothrops ja
27	277.5	18.7	604	13	Q9PT48	Q9PT48 atractaspis
28	273	18.4	616	13	Q90495	Q90495 echis carin
29	270	18.2	735	11	Q60411	Q60411 cavia porce
30	269.5	18.2	697	11	Q9R158	Q9R158 mus musculu
31	269.5	18.2	873	13	Q42595	Q42595 xenopus lae
32	268	18.1	419	13	Q92043	Q92043 crotalus at
33	267.5	18.0	857	4	Q9UHP2	Q9UHP2 homo sapien
34	267.5	18.0	918	4	Q9EH03	Q9EH03 homo sapien
35	267.5	18.0	918	4	Q9EBL5	Q9EBL5 homo sapien
36	267	18.0	1569	5	Q9VPH0	Q9VPH0 drosophila
37	262	17.7	761	11	Q9R160	Q9R160 mus musculu
38	261	17.6	788	11	Q35227	Q35227 mus musculu
39	259	17.5	451	13	Q9PT49	Q9PT49 atractaspis
40	257	17.3	505	13	Q73795	Q73795 agkistrodon
41	257	17.3	617	13	Q90499	Q90499 echis pyram
42	257	17.3	789	11	Q63180	Q63180 rattus norv
43	254	17.1	903	11	Q61824	Q61824 mus musculu
44	253	17.0	685	5	Q9VXL1	Q9VXL1 drosophila
45	253	17.0	694	5	Q9GZ15	Q9GZ15 drosophila

## ALIGNMENTS

RESULT 1

ID Q10742 PRELIMINARY: PRT: 691 AA.

AC Q10742: Q92650;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE DISINTEGRIN-METALLOPROTEASE MADM (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
NCBI\_Taxid:9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE:96276398; PubMed:8694785;  
RA Howard L., Lu X., Mitchell S., Griffiths S., Glynn P.;  
RT "Molecular cloning of MADM, a catalytically active mammalian  
RT disintegrin-metalloprotease expressed in various cell types.";  
RL Biochem. J. 317:45-50(1996).  
DR EMBL: Z48579; CA68463.1; -.  
DR HSSP: P18619; IFVL.  
DR MEROPS: M2.210; -.  
DR InterPro: IPR001762; Disintegrin.  
DR InterPro: IPR001590; Reprolysin.  
DR InterPro: IPR000130; Zn\_MTPeptide.  
DR Pfam: PF00200; disintegrin\_1.  
DR Pfam: PF01421; Reprolysin\_1.  
DR PRINTS: PR00289; DISINTEGRIN.  
DR SMART: SM00050; DISTIN\_1.  
DR PROSITE: PS50215; ADAM\_MEPRO\_1.  
DR PROSITE: PS50214; DISINTEGRIN\_2\_1.  
DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
KW Integrin.  
FT NON-TER  
SQ SEQUENCE 691 AA; 77632 MW; 8B4369F24B6B292 CRC64;

Query Match 99.2%; Score 1472; DB 4; Length 691;  
Best local Similarity 100.0%; Pred. No. 1.8e-131;  
Matches 262; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NSQNHDDYCLAAYFTDRDPEDDYGLAWGAPSGSGGICRKSRLYSGKKKSLNTGII 60

Db	247	NSQGNHDDYCLAYVFTRDPRDDYGLGLAMYGAPSSGGGICEKSKLYISQKGLKSLINIGII	306
Qy	61	TYQNGSHYPRKYSHTTAAHXYGINEGSSPHDSGTECTPEBSKYLQCKENGATIMYARTS	120
Db	307	TYQNGSHYPPYVSHLTTHAEHGXHFSSPHDSGTECTPEBSKYLQCKENGATIMYARTS	366
Qy	121	GDKLNNKFSILCSIRNISQVLEKKRNKCFVESGQPTIOGNMYEGEBCDCGYSDDCKDEC	180
Db	367	GDKLNNKFSILCSIRNISQVLEKKRNKCFVESGQPTIOGNMYEGEBCDCGYSDDCKDEC	426
Qy	181	CFPANDPEEGKCKLPGKQCSFSQPCCTQACAFKSKSEKGRDSDSCAREGJLNGFTALC	240
Db	427	CFPANDPEEGKCKLPGKQCSFSQPCCTQACAFKSKSEKGRDSDSCAREGJLNGFTALC	486
Qy	241	PASDPKPNFTDCNRHTQVCIING	262
Db	487	PASDPKPNFTDCNRHTQVCIING	508

RESULT	2			
ID	014672	PRELIMINARY:	PRT:	748 AA.
AC	014672:			
DT	01-JAN-1998 (TREMBLrel. 05)	Created		
DT	01-JAN-1998 (TREMBLrel. 05)	Last sequence update		
DT	01-JUN-2001 (TREMBLrel. 17)	Last annotation update		
DE	ADAM10.			
GN	ADAM10.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=97450992; PubMed=9305925;			
RA	Rosendahl M.S., Ko S.C., Long D.L., Brewer M.T., Rosenzweig B.,			
RA	Hodl E., Anderson L., Pyle S.M., Moreland J., Meyers M.A., Kohno T.,			
RA	Livons D., Liechtenstein H.S.;			
RT	Identification and characterization of a pro-tumor necrosis factor-			
RT	alpha-processing enzyme from the ADAM family of zinc			
RL	J. Biol. Chem. 272:24588-24593(1997).			
DR	EMBL; AF009615; AAC51766.1; -.			
DR	HSSP; P18619; 1FVL.			
DR	InterPro; IPR001762; DistIntegrin.			
DR	InterPro; IPR001590; Reprolysin.			
DR	InterPro; IPR000130; Zn_MMPeptide.			
DR	Pfam; PF00200; distIntegrin.1.			
DR	Pfam; PF01421; Reprolysin.1.			
DR	SMART; SM00050; DISIN.1.			
DR	PROSITE; PSS0215; ADAM_MERO.1.			
DR	PROSITE; PSS0214; DISTINTEGRIN.2.			
DR	PROSITE; PSS0142; ZINC_PROTEASE; UNKNOWN.1.			
SO	SEQUENCE 748 AA; 84142 MW; 08B1E65B17022A71 CRC64;			

	Query Match	99.2%	Score 1472;	DB 4;	length 748;
	Best Local Similarity	100.0%	Pred. 10e-131;		
	Matches 262;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps
QY	1	NSQBNHDDYCLAYVFTRDFDRFDGCVGLAWGAPSGSGGICERKSKLYSDGKKKSLNGLI	60		
Db	304	NSQBNHDDYCLAYVFTRDFDRFDGCVGLAWGAPSGSGGICERKSKLYSDGKKKSLNGLI	363		
QY	61	TVQNTSGSHVPKPKYSHITTFRAHEXGHNFGSPHDSGTECTPEGEKRNLCQKENGNTIMYRATRS	120		
Db	364	TVQNTSGSHVPKPKYSHITTFRAHEXGHNFGSPHDSGTECTPEGEKRNLCQKENGNTIMYRATRS	4233		
QY	121	GDKLNNKPSLCSIRNISOYLEKKRNKCPFESGQPTCGNGNVDGDEEDDCGSPQDCDEC	160		
Db	424	GDKLNNKPSLCSIRNISOYLEKKRNKCPFESGQPTCGNGNVDGDEEDDCGSPQDCDEC	4833		

Qy	Db	Qy	Db
181	CFPANDPEGRKCKLKGKQCSFSGPCCCTACAFKSKSEKCRDSDCAREGICNGPALT	241	PASPPEKPFITDCNRHTQVINC 262
484	CFDANDPEGRKCKLKGKQCSFSGPCCCTACAFKSKSEKCRDSDCAREGICNGPALT	544	PASPPEKPFITDCNRHTQVINC 565

RESULT	3			
ID	010743			
AC	010743;	PRELIMINARY;	PRT;	544 AA.
DT	01-NOV-1996 (TREMBLrel_01, Created)			
DT	01-NOV-1996 (TREMBLrel_01, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel_17, Last annotation update)			
DE	DISINTEGRIN-METALLOPROTEINASE PRECURSOR (CC 3.4.24.-) (MYELIN-ASSOCIATED			
DE	METALLOPROTEINASE) (MADN) (FRAGMENT).			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	[1] NCBI_Taxid=10116;			
RN				
RP	SEQUENCE FROM N.A.			
RC	STRATIN-SPRAGUE-DAWLEY; TISSUE=BRNIN;			
RX	MEDLINE=96276398; PubMed=8694795;			
RA	Howard L., Mitchell S., Lu X., Griffiths S., Glynn P.;			
RT	"Molecular cloning of MADN: a catalytically active mammalian			
RT	disintegrin-metallprotease expressed in various cell types."			
RL	Biochem. J. 317:45-50(1996).			
CC	-1- SUBCELLULAR LOCATION: INTEGRIN MEMBRANE PROTEIN.			
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B (ZINC			
CC	METALLOPROTEASE); ALSO KNOWN AS THE REPOLYSIN SUBFAMILY.			
CC	-1- SIMILARITY: HIGH IN THE MIDDLE REGION, NO DISINTEGRINS.			
DR	EMBL; Z48444; CA88359.1; -.			
DR	HSSP; P18619; IFVL.			
DR	MEROPS; M12.210; -.			
DR	InterPro; IPR001762; Disintegrin.			
DR	InterPro; IPR001590; Repolysin.			
DR	InterPro; IPR000130; Zn_MTPetase.			
DR	Pfam; PF00200; disintegrin.1.			
DR	Pfam; PR01421; Repolysin.1.			
DR	PRINTS; PRO0289; DISINTEGRIN.			
DR	SMART; SM00050; DISTRN.1.			
DR	PROSITE; PS50215; ADAM_MERPO.1.			
DR	PROSITE; PS50214; DISINTEGRIN_2.1.			
DR	PROSITE; PS00142; ZINC_PROTEASE. UNKNOWN.1.			
KN	Integrin; Hydrolase; Metalloprotease; Transmembrane; Zinc; Signal;			
KW	Glycoprotein.			
FT	NON-TER	1		
FT	SIGNAL	<1	9	
FT	CHAIN	10	241	
FT	CHAIN	242	346	
FT	DOMAIN	10	468	
FT	TRANSMEM	469	492	
FT	DOMAIN	493	544	
FT	ACT_SITE	180		
FT	METAL	179	180	
FT	METAL	179	179	
FT	METAL	183	183	
FT	METAL	189	189	
FT	CARBOHYD	63	63	
FT	CARBOHYD	74	74	
FT	CARBOHYD	235	235	
FT	CARBOHYD	347	347	
FT	SEQUNCE	544 AA;	60444 MW;	F75E08BDC88A7DD CRC64;

Query Match	98.88	Score 1466	DB 11	Length 544
Best Local Similarity	99.28	Pred. No. 5.1e-131		
Matches 260	Conservative	2	Mismatches 0	Indels 0
			Gaps 0	
Qy	1	NSEGNHDDYCLAVFVDRPDGCVGLCAVACGAPSSSSGICIEKKRLYSDCKKKSINTGII	60	

DB 100 NSEONHDDYCLAYFTDRDDEDDVGLAWGAPSSGGICSEKSLYSDGKKSLNTGII 159

QY 61 TVQNGSHVPRKSHITFAHEVGHNEGSPHDSCTECTPEESKLNLOKENGNTIMARATS 120

DB 160 TVQNGSHVPRKSHITFAHEVGHNEGSPHDSCTECTPEESKLNLOKENGNTIMARATS 219

QY 121 GDLKNNKFSICSIRNISQVLEKRRNRCFVESGOPICGNGMYEOGEECDGCGSDQCKDEC 180

DB 220 GDLKNNKFSICSIRNISQVLEKRRNRCFVESGOPICGNGMYEOGEECDGCGSDQCKDEC 279

QY 181 CPDANQPEGRKCKLPKQKQSPSGPCTAQCFAFKSKSEKCRDSDCAKEGICNGFTALC 240

DB 280 CPDANQPEGRKCKLPKQKQSPSGPCTAQCFAFKSKSEKCRDSDCAKEGICNGFTALC 339

QY 241 PASDPKPNFTDCNRRHTQVCING 262

DB 340 PASDPKPNFTDCNRRHTQVCING 361

RESULT 4

035598 PRELIMINARY; PRT; 749 AA.

ID 035598

AC 035598;

DT 01-JAN-1998 (TREMblrel. 05, Created)

DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)

DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)

DE KUZBANIAN

CN ADAM10 OR MKU2.

OC Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI\_Taxid=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97386452; PubMed=9244301;

RA Pan D., Rubin G.M.;

RT "Kuzbanian controls proteolytic processing of Notch and mediates lateral inhibition during Drosophila and vertebrate neurogenesis.";

RT Cell 90:271-280(1997).

DR EMBL; AF011379; AAC53303.1; -

DR HSSP; P18619; IFLV.

DR MEROPS; M12.211; -

DR MGD; MGI:109548; Adam10.

DR InterPro; IPR001762; Disintegrin.

DR InterPro; IPR001590; Reptolysin.

DR InterPro; IPR000130; Zn\_MTPeptide.

DR Pfam; PF00200; disintegrin; 1.

DR Pfam; PF01421; Reptolysin; 1.

DR SMART; SM00050; Disin; 1.

DR PROSITE; PS50215; ADAM\_MEROP; 1.

DR PROSITE; PS50214; DISINTEGRIN\_2; 1.

DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN\_1.

DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN\_1.

SO SEQUENCE 749 AA; 8396 MW; 06CEC3EB2C5F4F94 CRC64;

Query Match 98.6%; Score 1463; DB 11; Length 749;

Best Local Similarity 98.9%; Pred. No. 1.4e-130;

Matches 259; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

DB 485 CPDANQPEGRKCKLPKQKQSPSGPCTAQCFAFKSKSEKCRDSDCAKEGICNGFTALC 544

QY 241 PASDPKPNFTDCNRRHTQVCING 262

DB 545 PASDPKPNFTDCNRRHTQVCING 566

RESULT 5

010741 PRELIMINARY; PRT; 748 AA.

ID 010741

AC 010741;

DT 01-NOV-1996 (TREMblrel. 01, Created)

DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)

DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)

DE DISINTEGRIN-METALLOPROTEASE PRECURSOR (EC 3.4.24.-) (MYELIN-ASSOCIATED DE METALLOPROTEINASE) (MADM).

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI\_Taxid=9913;

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE-BRAIN:

RX MEDLINE=96276398; PubMed=8694785;

RA Howard L., Lu X., Mitchell S., Griffiths S., Glynn P.;

RT "Molecular cloning of MADM: a catalytically active mammalian disintegrin-metalloprotease expressed in various cell types.";

RT Biochem. J. 317:45-50(1996).

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN BRAIN. AT LOWER LEVELS IN KIDNEY, SPLEEN, LUNG AND HEART.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12C (ZINC METALLOPROTEASE).

CC -1- SIMILARITY: HIGH, IN THE MIDDLE REGION, TO DISINTEGRINS.

DR EMBL; Z21961; CAI79973.1; -

DR HSSP; P18619; IFLV.

DR MEROPS; M12.210; -

DR InterPro; IPR001762; Disintegrin.

DR InterPro; IPR001590; Reptolysin.

DR InterPro; IPR000130; Zn\_MTPeptide.

DR Pfam; PF00200; disintegrin; 1.

DR Pfam; PF01421; Reptolysin; 1.

DR SMART; SM00050; Disin; 1.

DR PROSITE; PS50215; ADAM\_MEROP; 1.

DR PROSITE; PS50214; DISINTEGRIN\_2; 1.

DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN\_1.

DR Integrin; Hydrolase; Metalloprotease; Transmembrane; zinc; Signal;

KW Glycoprotein.

FT SIGNAL 1 19

FT PROPEP 20 213

FT CHAIN 214 455

FT CHAIN 456 550

FT DOMAIN 20 672

FT TRANSDEM 673 696

FT DOMAIN 697 748

FT ACT\_SITE 384 384

FT METAL 383 383

FT METAL 387 387

FT METAL 393 393

FT CARBOHYD 267 267

FT CARBOHYD 278 278

FT CARBOHYD 439 439

FT CARBOHYD 551 551

SO SEQUENCE 748 AA; 84188 MW; 20ZE29830611FE9E1 CRC64;

Query Match 97.6%; Score 1449; DB 6; Length 748;

Best Local Similarity 97.7%; Pred. No. 3e-129;

Matches 256; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

DB 304 NSEQNHDDYCLAYFTDRDPPDGLGLAWGAPSGSSGICPKSKLYSDGKKSLNTGII 363  
 QY 61 TVQNGSHVPPKVSHTFAHEVGHNFSGPHDSGTECTPEESKNLQKENGWYIYARATS 120  
 DB 364 TVQNGSHVPPKVSHTFAHEVGHNFSGPHDSGTECTPEESKNLQKENGWYIYARATS 423  
 QY 121 GDKLNKNNFSLCSIRNISOYLEKKRNKNCVESGQPICGNGWEGEEDCCYSQDCDEC 180  
 DB 424 GDKLNKNNFSLCSIRNISOYLEKKRNKNCVESGQPICGNGWEGEEDCCYSQDCDEC 483  
 QY 181 CPDANQPGKCKLTKPKQCSPSQSGPCCCTAQCASFSSKSKCKDSDCARBICNGFTALC 240  
 DB 484 CYDANQPGKCKLTKPKQCSPSQSGPCCCTAQCASFSSKSKCKDSDCARBICNGFTALC 543  
 QY 241 PASDPKPNFTDCNRHTQVING 262  
 DB 544 PASDPKPNFTDCNRHTQVING 565  
 RESULT 6  
 Q9VA12 PRELIMINARY; PRT; 1537 AA.  
 ID Q9VA12:  
 AC 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE CG1964 PROTEIN.  
 GN CG1964.  
 OS Drosophila melanogaster (fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 RN NCBI\_TaxID=7227;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY.  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,  
 RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.G., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieres S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibbegan C.,  
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,  
 RA Laake P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Modyarty C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shie B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spredling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,

RT "The genome sequence of Drosophila melanogaster."  
 RL Science 287:2185-2195(2000).  
 CC -1- SIMILARITY: TO NEUTRAL ZINC METALLOPEPTIDASES, ZINC-BINDING REGION  
 CC DOMAIN.  
 DR EMBL: AE003770; AAF56926.1; .  
 DR HSSP: P18619; 1FV1.  
 DR FLYBase: FBgn0039688; CG1964.  
 DR InterPro: IPR001762; Disintegrin.  
 DR InterPro: IPR001590; Reprilysin.  
 DR InterPro: IPR000130; Zn\_Mtpeptase.  
 DR Pfam: PF01421; Reprilysin; 1.  
 DR SMART: SM00050; DISIN; 1.  
 DR PROSITE: PS50215; ADAM\_MEPRO; 2.  
 DR PROSITE: PS50214; DISINTEGRIN; 2; 1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; 1.  
 KW Hydrolase; Metalloprotease; Zinc.  
 SO SEQUENCE 1537 AA; 168796 MW; 46A52344A8E73617 CMC64;  
 Query Match 50.8%; Score 754; DB 5; Length 1537;  
 Best Local Similarity 54.3%; Pred. No. 6,2e-63;  
 Matches 145; Conservative 33; Mismatches 71; Indels 18; Gaps 9;  
 QY 2 SEQNHDDYCLAYFTDRDPPDGLGLAWGAPSGSGGICPKSKLYSDGKKSLNTGII 61  
 DB 566 SEEDYDFCLAYFTYDRDEMGTLGANTG-DLNAGGVCCKNHYR-GSLKSLNTGIYV 623  
 QY 62 VQNGSHVPPKVSHTFAHEVGHNFSGPHDSGTECTPEESKNLQKENGWYIYARATSG 121  
 DB 624 LLNKGKHPAPVAVSHVLAHEIGHNFGSPHDP-EQCTP6-----GEGDNFIMFARATSG 675  
 QY 122 DKLNNKFSLSIRNISOYLEKKRNKNCVESGQPICGNGWEGEEDCCYSQDCDEC 178  
 DB 676 DKKNNKFSLSLSKLEPLNLNKAISMKGCFTEPOSSICGNGVYEPQDCDEEDCKD 735  
 QY 179 ECGFD-ANQP--EGKCKLTKPKQCSPSQSGPCCCTAQCASFSSKSKCKDSDCARBICNG 235  
 DB 736 SCCPMRSQRLDERCTLTLPARCSPSQSGPCCCTTCKLKP-GDKCRDMDGCRDPSFCOG 794  
 QY 236 FTALCPASDPKPNFTDCNRHTQVING 262  
 DB 795 RVPCGPPSVAKPKKTIICNNEF-VCIWG 820  
 RESULT 7  
 Q9NKF9 PRELIMINARY; PRT; 1236 AA.  
 ID Q9NKF9:  
 AC 09NKF9;  
 DT 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE K02 PROTEIN.  
 GN K02 OR B6:DS07660.3 OR CG1747.  
 OS Drosophila melanogaster (fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 RN NCBI\_TaxID=7227;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Y, CN BW SP;  
 RX MEDLINE=99403001; PubMed=10471707;  
 RA Ashburner M., Miska S., Roote J., Lewis S.E., Blazer R., Davis T.,  
 RA Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,  
 RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,  
 RA Palazolo M., Reese M.G., Spredling A., Tsang G., Wan K., Whitelaw K.,  
 RA Celniker S., Rubin G.M.,  
 RT "An exploration of the sequence of a 2.9-kb region of the genome of  
 Drosophila melanogaster: the Adh region."  
 RL Genetics 153:179-219(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Y, CN BW SP;

QY	1	NSQNDHDXCLAYVTFFDDFDGVLGLAWGASGSSGGICRKSIVSD-----GRKK	53
Db	518	HSLEDHSDCLAYVTFFDDFDGVLGLAWAASASGASGGICRKYTYETVETWGGQYQSTR	577
QY	54	SLNPGIITVQNGSGVPPKVSHTFFAHFVHNGSPHSDGCTCTGEBEKNIGKQENKENTY	113
Db	578	SLNPGIITVYNTNSRPAPKVSQTLTAHIGHNFSGPHDPOECPRGGL-----NONT	630
QY	114	MYRATSGDKLNNKPFSLCIRNISOYLE---KRNKNCVYESGQPIGNGMVEQGEED	169
Db	631	MFSATSGDRPNNSKPFSCIRINISNVLVDLVGNCTFRDCKFKASEGAFECGNKIYVSGEED	690
QY	170	CGAS-DOCKDECCF-----DANOEGRKCKLKRGKQCSPOGPGCTTA-QCAF---KSK	217
Db	691	CGRNEBECKDKCICYRLLISEYDQSIANSAGCGRRAKTCQSSQGPCLSLNSCFTPTSV	750
QY	218	SEKCRDSDCAREGICNGFTALCPASDPKKNFTDCRKHQYCSG	262
Db	751	HQCKEETRECSWSSCTNCTGTACPEPRHRDDKTMCMNNGTALCIRG	795
RESULT	9		
ID	094902		
AC	094902	PRELIMINARY;	PRT; 1239 AA.
DT	01-FEB-1997 (TREMblrel. 02, Created)		
DT	01-FEB-1997 (TREMblrel. 02, Last sequence update)		





OS Naja naja (Indian cobra).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 CC Elapidae; Elapinae; Naja.  
 CC NCBI\_TaxID=35670;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=KAOUTHA; TISSUE=VENOM GLAND;  
 RA Bambi B., Bredehorst R., Vogel C.-W.;  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF063190; AAF00693.1; -  
 DR HSSP: P1494; 1KST.  
 DR InterPro: IPR001762; Disintegrin.  
 DR InterPro: IPR002870; Pep\_M12B\_propep.  
 DR InterPro: IPR001590; Reprolysin.  
 DR InterPro: IPR000130; Zn\_MTPepidase.  
 DR Pfam: PF00200; disintegrin\_1.  
 DR Pfam: PF01562; Pep\_M12B\_propep\_1.  
 DR Pfam: PF01421; Reprolysin\_1.  
 DR PRINTS: PR00289; Disintegrin.  
 DR ProDom: PD000664; Disintegrin\_1.  
 DR SMART: SM00050; DISIN\_1.  
 DR PROSITE: PS50215; ADAM\_MEPRO\_1.  
 DR PROSITE: PS50214; DISINTEGRIN\_2; 1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
 KW Signal.  
 FT SIGNAL 1 6 POTENTIAL.  
 FT CHAIN 180 600 COBRIN.  
 FT FT  
 SQ SEQUENCE 600 AA; 67661 MW; C7C0D45EBC694290 CRC64;  
 Query Match 20.1%; Score 298.5; DB 13; Length 600;  
 Best Local Similarity 31.3%; Pred. No. 3,8e-20;  
 Matches 81; Conservative 27; Mismatches 98; Indels 53; Gaps 11;  
 QY 12 AYVTDDEDDVGLAWGAPSGSGGICEKSKLYSGKKSLNTGIIYONGSHVPP 71  
 DB 282 AQLTGTIDFNGTVPGLAYIGS-----ICNP-----KTSAAVQDSKST-- 320  
 QY 72 KVSHTFAHEVGHNFSGSPHDSGTECTPGESKMLGQKENGNTIMYARATSGDKLNKNSFL 131  
 DB 321 RMVAITVAHEGHNLGMNDKGF-CTCGFNK-----CVMSTRRTK---PAYQFSS 366  
 QY 132 CSTINISGOVLEKRRNCFVES-----GPTICGNMYEGEEDDCGSDQCKDECCFPA 184  
 DB 367 CSVREHORVILRDPPQCTILNKPLSTDIYSPICGNFYVVEGECDCSPADQSQACC--- 423  
 QY 185 NQPEGRCKLKPQKCSFSGPCTAOCAPKSKSEKRD-DSDCAREGICNGFTALCPAS 243  
 DB 424 ---NATTCCKLOHEAQCDSE---CCEKCKFKGAGACRAKDDCLPELCTGSAECPTD 477  
 QY 244 DPKNFTDCNRHVOYVING 262  
 DB 478 VFQRNGLPC-ONNGCYING 495  
 RESULT 15  
 042138 PRELIMINARY; PRT: 620 AA.  
 AC 042138:  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE METALLOPROTEINASE-DISINTEGRIN-LIKE PROTEIN (EC 3.4.24.-).  
 OS Agkistrodon confortix latiductus.  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 CC Viperidae; Crotalinae; Agkistrodon.  
 CC NCBI\_TaxID=37195;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=98052412; PubMed=9392519;  
 RA Seifstine De Araujo H.S., de Souza D.H., Ombay C.L.;

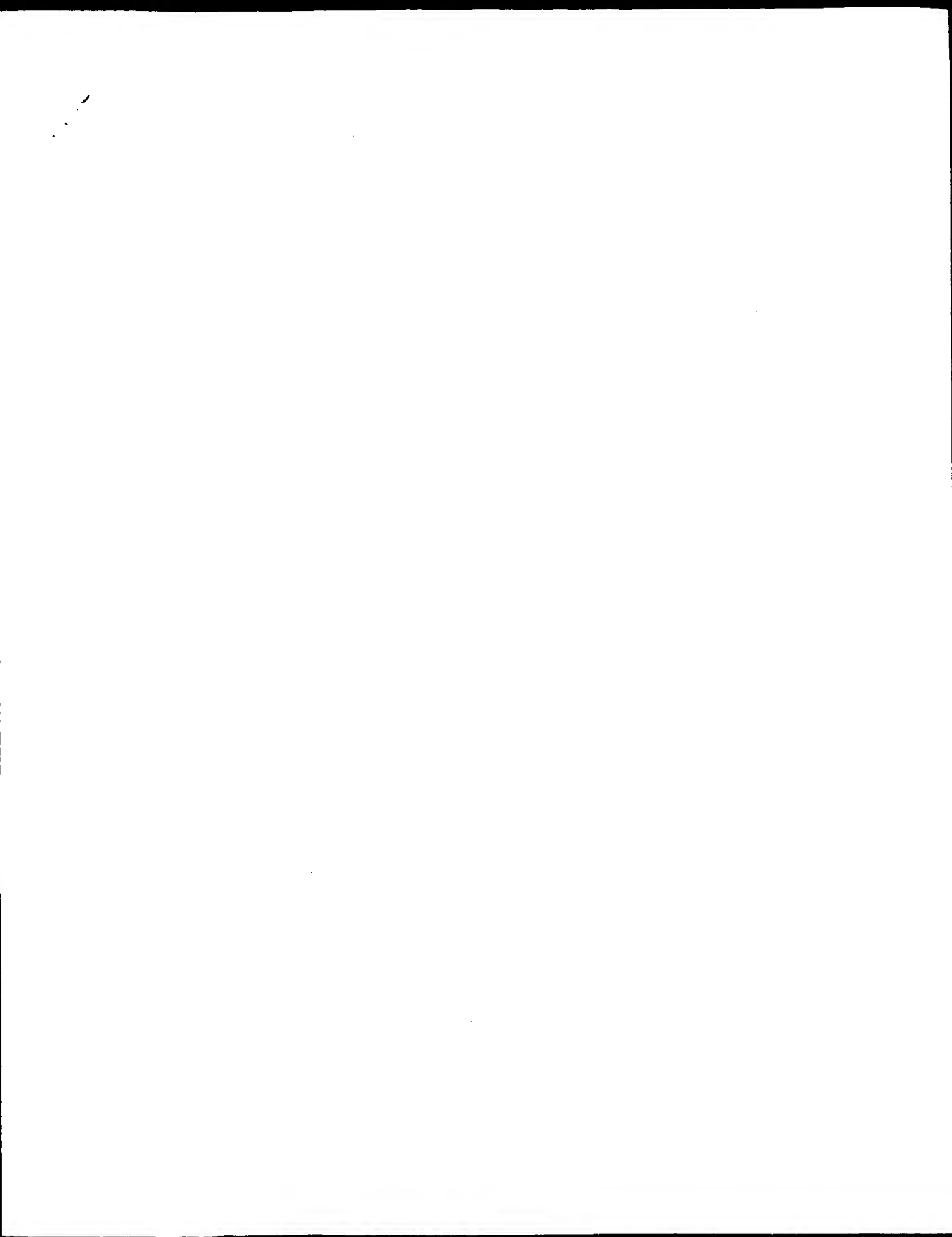
RT "Analysis of a cDNA sequence encoding a novel member of the snake  
 RT venom metalloproteinase, disintegrin-like, cysteine-rich (MOC) protein  
 RT family from Agkistrodon confortix latiductus."  
 RL Biochim. Biophys. Acta 1342:109-115(1997).  
 CC -1- SIMILARITY: CONTAINS A DISINTEGRIN DOMAIN.  
 DR EMBL: U86634; AAC18911.1; -  
 DR HSSP: P18619; 1FVL.  
 DR InterPro: IPR001762; Disintegrin.  
 DR InterPro: IPR002870; Pep\_M12B\_propep.  
 DR InterPro: IPR001590; Reprolysin.  
 DR InterPro: IPR000130; Zn\_MTPepidase.  
 DR Pfam: PF00200; disintegrin\_1.  
 DR Pfam: PF01562; Pep\_M12B\_propep\_1.  
 DR Pfam: PF01421; Reprolysin\_1.  
 DR PRINTS: PR00289; Disintegrin.  
 DR ProDom: PD000664; Disintegrin\_1.  
 DR SMART: SM00050; DISIN\_1.  
 DR PROSITE: PS50215; ADAM\_MEPRO\_1.  
 DR PROSITE: PS50214; DISINTEGRIN\_2; 1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
 KW Hydrolase; protease; Metalloprotease; Zinc; Venom; Zymogen.  
 SQ SEQUENCE 620 AA; 69512 MW; 9016AFEB5AE0BB87 CRC64;

Query Match 19.7%; Score 293; DB 13; Length 620;  
 Best Local Similarity 29.7%; Pred. No. 1,3e-19;  
 Matches 79; Conservative 37; Mismatches 96; Indels 54; Gaps 13;  
 QY 4 QNHDDYCLAVFTDRDDEDDVGLAWGAPSGSGGICEKSKLYSGKKSLNTGIIYVQ 63  
 DB 283 KSHDN---AQLTGTIDFNGTVPGLAYIGS-----ICNP-----KTSAAVQDSKST-- 320  
 QY 64 NGSHPVSHHTFAHEVGHNFSGSPHDSGTECTPGESKMLGQKENGNTIMYARATSGDK 123  
 DB 321 DHST--INLMNAVITVAHEGHNLGMNDKGF-CTCGFNK-----CVMSTRRTK---PAYQFSS 366  
 QY 124 LNNKFSLSIRNISOVLEKRRNCFVES-----GPTICGNMYEGEEDDCGSDQCK 176  
 DB 366 QPKLFNSQSDYRKYLLKRRPKCLINEPNTDIYSPICGNFYVVEGECDCSPADQSQACC--- 423  
 QY 177 KDECCFDANQPEGRCKLKPQKCSFSGPCTAOCAPKSKSEKRD-DSDCAREGICNG 235  
 DB 426 QNPCC-----DAATCKLPLPSQC--ADGVCCD-QCFRTAGTECRQAKDDCDMDLCTG 476  
 QY 236 FTALCPASDPKRFVDCNRHVOYVING 261  
 DB 477 QSAECPTDRFQRNGHPCPLDNGCYTN 502

Search completed: April 1, 2002, 15:12:07  
 Job time: 689 sec

Mon Apr 1 15:19:29 2002

us-09-871-388-6.rsp



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: April 1, 2002, 15:12:07 ; Search time 98.78 Seconds

(Without alignments)  
1109.111 Million cell updates/sec

Title: us-09-871-388-8

Sequence: 4103 1 MVLPTVLLILLSMAAGLGGO.....IQPPROPRESYQMGHMR 749

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 segs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: SP archaea:\*  
2: SP bacteria:\*  
3: SP fungi:\*  
4: SP human:\*  
5: SP\_invertebrate:\*  
6: SP\_mammal:\*  
7: SP\_mmc:\*  
8: SP\_organelle:\*  
9: SP\_phage:\*  
10: SP\_plant:\*  
11: SP\_rodent:\*  
12: SP\_virus:\*  
13: SP\_vertebrate:\*  
14: SP\_unclassified:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4103	100.0	749	11	O35598
2	3940.5	96.0	748	6	O14672
3	3884.5	94.7	748	6	O10741
4	3346	81.6	691	4	O10742
5	2956	72.0	544	11	O10743
6	1489.5	36.3	1238	5	O9VIM9
7	1409	36.3	1239	5	O9A902
8	1487.5	36.3	1236	5	O9NMF9
9	1397	34.0	922	5	O46354
10	1332	33.0	1537	5	O9VA12
11	707	17.2	162	13	O42568
12	478	11.7	686	5	O9A316
13	416.5	10.2	845	11	O61072
14	409	10.0	600	13	O9PVK7
15	406	9.9	75	6	O77633
16	395.5	9.6	819	4	O13443
17	385	9.4	616	13	O90495
18	384.5	9.4	604	13	O9PT48
19	380.5	9.3	873	13	O42595

20	377.5	9.2	610	13	O9DGB9
21	375	9.1	914	13	O12960
22	372	9.1	620	13	O42138
23	365	8.9	735	11	O60411
24	361.5	8.8	920	11	O35674
25	360	8.8	617	13	O90499
26	351.5	8.6	728	4	O9B211
27	350	8.5	609	13	O90282
28	348	8.5	505	13	O73795
29	345.5	8.4	606	13	O98UF9
30	345.5	8.4	610	13	O9Y120
31	343.5	8.2	609	13	O9W6M5
32	337.5	8.2	1569	5	O9VPH0
33	337	8.2	760	11	O9DAE4
34	337	8.2	918	4	O9B013
35	337	8.2	918	4	O9B215
36	333.5	8.1	610	13	O93523
37	333	8.1	760	11	O9R159
38	332.5	8.1	832	4	O75077
39	329.5	8.0	829	11	O9R1V7
40	328	8.0	697	11	O9R158
41	326	7.9	419	13	O92043
42	324.5	7.9	549	13	O90500
43	324.5	7.9	857	4	O9UHP2
44	323.5	7.9	903	11	O61824
45	323	7.9	739	4	O9Y3Q7

## ALIGNMENTS

```
RESULT 1
O35598 PRELIMINARY; PRT: 749 AA.
AC O35598:
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE KUZBANIAN.
OS ADAM10 OR MKU2.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97386452; PubMed=9244301;
RA Pan D., Rubin G.M.;
RT "Kuzbanian controls proteolytic processing of Notch and mediates
RT lateral inhibition during Drosophila and vertebrate neurogenesis.";
RL Cell 90:271-280(1997).
DR EMBL: AF011379; AAC53303.1; -.
DR HSP: P18619; LEVL.
DR MEROPS: M12.211; -.
DR MGD: MGI:109548; Adam10.
DR InterPro: IPR001762; Disintegrin.
DR InterPro: IPR001590; Repolysin.
DR InterPro: IPR000130; Zn_MTPetase.
DR Pfam: PF00200; disintegrin; 1.
DR Pfam: PF01421; Repolysin; 1.
DR SMART: SM00050; DISTRN; 1.
DR PROSITE: PS02015; ADAM_MEROP; 1.
DR PROSITE: PS0214; DISINTEGRIN_2; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN; 1.
SQ SEQUENCE 749 AA; 83966 MW; 06CC3CB2C5FAFF94 CRC64;

Query Match 100.0%; Score 4103; DB 11; Length 749;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 749; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MVLPTVLLLSMAAGLGQYGNPLNKYIRHYEGSLYNVDSLHOKHOKRAVSHEDQFL 60
QY 61 LLDFFAHGROFNLRMKRDSTLSDEFKETSNNKYLDVDTSHIYTHGHIYGEESFSGSVI 120
Db 61 LLDFFAHGROFNLRMKRDSTLSDEFKETSNNKYLDVDTSHIYTHGHIYGEESFSGSVI 120
QY 121 DGRFEGFIKTRGTFYIEPARYIKDRLLPFHSYIYHEDDINYPHKYGGGACADHSYFE 180
Db 121 DGRFEGFIKTRGTFYIEPARYIKDRLLPFHSYIYHEDDINYPHKYGGGACADHSYFE 180
QY 181 RMKRYOMTGVGEERARHPEKHAASGPPELLRKRRTTLAERNTOCLYIQDHLFFKYGYR 240
Db 181 RMKRYOMTGVGEERARHPEKHAASGPPELLRKRRTTLAERNTOCLYIQDHLFFKYGYR 240
QY 241 EAVIAOISSHVAKIDITYOTDFSGIRNISFMVKRIRINTSDEKPTNPREPNIGVEK 300
Db 241 EAVIAOISSHVAKIDITYOTDFSGIRNISFMVKRIRINTSDEKPTNPREPNIGVEK 300
QY 301 FLELSEQNHHDDYCLAYVETDRDGDVGLAWGAPSGSGGICEKSKLYSDGKKSLN 360
Db 301 FLELSEQNHHDDYCLAYVETDRDGDVGLAWGAPSGSGGICEKSKLYSDGKKSLN 360
QY 361 TGIITVQNGSHVPPKVSHTFPAHEVGHNGFSPHDSGTECTPESKNLQKENGNYIYTA 420
Db 361 TGIITVQNGSHVPPKVSHTFPAHEVGHNGFSPHDSGTECTPESKNLQKENGNYIYTA 420
QY 421 RATSQKLNNNKFSICSTIRNISQVLEKRRNCFVESGPTCGNGNVEGECDCGYSDOC 480
Db 421 RATSQKLNNNKFSICSTIRNISQVLEKRRNCFVESGPTCGNGNVEGECDCGYSDOC 480
QY 481 KDDCCFDANOPREGKCKLPGKQCSPOGCTAQCFAFKSKSEKCRDSDCAKEGICNGF 540
Db 481 KDDCCFDANOPREGKCKLPGKQCSPOGCTAQCFAFKSKSEKCRDSDCAKEGICNGF 540
QY 541 TALCPASDPKPNFTDCNHRHTQVINGOCAGSICEKYDLEECTASSDGKKNELCHVCM 600
Db 541 TALCPASDPKPNFTDCNHRHTQVINGOCAGSICEKYDLEECTASSDGKKNELCHVCM 600
QY 601 KKAAPSTCASTGSLQMSKQFSGRTITLQPGSPCNDPFCQCDVFMKRLVDADGLARLKK 660
Db 601 KKAAPSTCASTGSLQMSKQFSGRTITLQPGSPCNDPFCQCDVFMKRLVDADGLARLKK 660
QY 661 AIFSPOLYENIAEWIVAHMVAVLLMGLALIMLAGFIKICSVHTSPSNPKLPPKPLPGT 720
Db 661 AIFSPOLYENIAEWIVAHMVAVLLMGLALIMLAGFIKICSVHTSPSNPKLPPKPLPGT 720
QY 721 LKRRRPPQIOPPRQRPRESYOMGHMR 749
Db 721 LKRRRPPQIOPPRQRPRESYOMGHMR 749

RESULT 2
014672 PRELIMINARY: PRT: 748 AA.
AC 014672;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE ADAM10.
CN ADAM10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI:TaxID-9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE-97450992; PubMed-9305925;
RA Rosendahl M.S., Ko S.C., Long D.L., Brewer M.T., Rosenzweig B.,
RA Lyons D., Liebenstein H.S.;
RA "Identification and characterization of a pro-tumor necrosis factor-
RT alpha-processing enzyme from the ADAM family of zinc
RT metalloproteases."

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RL J. Biol. Chem. 272:24588-24593 (1997).
DR EMBL: AF009615; AAC51766.1; -.
DR HSSP: P18619; 1FVJ.
DR InterPro: IPR001762; Distintegrin.
DR InterPro: IPR001590; Repolysin.
DR Pfam: PF00200; distintegrin.
DR Pfam: PF01421; Repolysin.
DR SMART: SM00050; DISIN.
DR PROSITE: PS50215; ADAM_MEPRO.
DR PROSITE: PS50214; ZINC_PROTEASE.
DR PROSITE: PS00142; ZINC_PROTEASE.
SQ SEQUENCE 748 AA: 84142 MW: 088165817022471 CRC64:

Query Match          96.0%; Score 3940.5; DB 4; Length 748;
Best local similarity 95.9%; Pred. No. 0;
Matches 718; Conservative 15; Mismatches 15; Indels 1; Gaps 1;

QY 1 MVLPTVLLLSMAAGLGQYGNPLNKYIRHYEGSLYNVDSLHOKHOKRAVSHEDQFL 60
Db 1 MVLPTVLLLSMAAGLGQYGNPLNKYIRHYEGSLYNVDSLHOKHOKRAVSHEDQFL 60
QY 61 LLDFFAHGROFNLRMKRDSTLSDEFKETSNNKYLDVDTSHIYTHGHIYGEESFSGSVI 120
Db 61 LLDFFAHGROFNLRMKRDSTLSDEFKETSNNKYLDVDTSHIYTHGHIYGEESFSGSVI 120
QY 121 DGRFEGFIKTRGTFYIEPARYIKDRLLPFHSYIYHEDDINYPHKYGGGACADHSYFE 180
Db 121 DGRFEGFIKTRGTFYIEPARYIKDRLLPFHSYIYHEDDINYPHKYGGGACADHSYFE 180
QY 181 RMKRYOMTGVGEERARHPEKHAASGPPELLRKRRTTLAERNTOCLYIQDHLFFKYGYR 240
Db 181 RMKRYOMTGVGEERARHPEKHAASGPPELLRKRRTTLAERNTOCLYIQDHLFFKYGYR 240
QY 241 EAVIAOISSHVAKIDITYOTDFSGIRNISFMVKRIRINTSDEKPTNPREPNIGVEK 300
Db 241 EAVIAOISSHVAKIDITYOTDFSGIRNISFMVKRIRINTSDEKPTNPREPNIGVEK 300
QY 301 FLELSEQNHHDDYCLAYVETDRDGDVGLAWGAPSGSGGICEKSKLYSDGKKSLN 360
Db 301 FLELSEQNHHDDYCLAYVETDRDGDVGLAWGAPSGSGGICEKSKLYSDGKKSLN 360
QY 361 TGIITVQNGSHVPPKVSHTFPAHEVGHNGFSPHDSGTECTPESKNLQKENGNYIYTA 420
Db 361 TGIITVQNGSHVPPKVSHTFPAHEVGHNGFSPHDSGTECTPESKNLQKENGNYIYTA 420
QY 421 RATSQKLNNNKFSICSTIRNISQVLEKRRNCFVESGPTCGNGNVEGECDCGYSDOC 480
Db 421 RATSQKLNNNKFSICSTIRNISQVLEKRRNCFVESGPTCGNGNVEGECDCGYSDOC 480
QY 481 KDDCCFDANOPREGKCKLPGKQCSPOGCTAQCFAFKSKSKCKDSDCAKEGICNGF 540
Db 481 KDDCCFDANOPREGKCKLPGKQCSPOGCTAQCFAFKSKSKCKDSDCAKEGICNGF 540
QY 541 TALCPASDPKPNFTDCNHRHTQVINGOCAGSICEKYDLEECTASSDGKKNELCHVCM 600
Db 541 TALCPASDPKPNFTDCNHRHTQVINGOCAGSICEKYDLEECTASSDGKKNELCHVCM 600
QY 601 KKAAPSTCASTGSLQMSKQFSGRTITLQPGSPCNDPFCQCDVFMKRLVDADGLARLKK 660
Db 601 KKAAPSTCASTGSLQMSKQFSGRTITLQPGSPCNDPFCQCDVFMKRLVDADGLARLKK 660
QY 661 AIFSPOLYENIAEWIVAHMVAVLLMGLALIMLAGFIKICSVHTSPSNPKLPPKPLPGT 720
Db 661 AIFSPOLYENIAEWIVAHMVAVLLMGLALIMLAGFIKICSVHTSPSNPKLPPKPLPGT 720
QY 721 LKRRRPPQIOPPRQRPRESYOMGHMR 749
Db 721 LKRRRPPQIOPPRQRPRESYOMGHMR 749

RESULT 3

```

010741 PRELIMINARY: PRT: 748 AA.

AC 010741:

DT 01-NOV-1996 (TREMBLER, 01, Created)

DT 01-NOV-1996 (TREMBLER, 01, Last sequence update)

DE 01-JUN-2001 (TREMBLER, 17, Last annotation update)

DE DISINTEGRIN-METALLOPROTEASE PRECURSOR (EC 3.4.24.-) (MYELIN-ASSOCIATED METALLOPROTEINASE) (MAMM).

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.

OX NCBI\_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.

RC TISSUE-BRAIN:

RX MEDLINE=96276398; PubMed=8694785;

RA Howard L., Lu X., Mitchell S., Griffiths S., Glynn P.;

RT "Molecular cloning of MAMM: a catalytically active mammalian disintegrin-metalloprotease expressed in various cell types.";

RT Biochem. J. 317:45-50(1996).

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN BRAIN. AT LOWER LEVELS IN KIDNEY, SPLEEN, LUNG AND HEART.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2C (ZINC METALLOPROTEASE).

CC -1- SIMILARITY: HIGH, IN THE MIDDLE REGION, TO DISINTEGRINS.

CC EMBL: Z21861; CAAT9973.1; -.

DR DR HESP; P18619; IFLV.

DR DR MERO; M12.210; -.

DR DR InterPro: IPR001762; Disintegrin.

DR InterPro: IPR001590; Repolysin.

DR InterPro: IPR000130; Zn\_MTPeptide.

DR Pfam: PF00200; disintegrin\_1.

DR Pfam: PF01421; Repolysin; 1.

DR SMART; SM00050; Disin; 1.

DR PROSITE; PS50215; ADAM\_MERO; 1.

DR PROSITE; PS50214; DISINTEGRIN\_2; 1.

DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN; 1.

KW Integrin; Hydrolase; Metalloprotease; Transmembrane; Zinc; Signal;

KW Glycoprotein.

FT SIGNAL 1 19 POTENTIAL.

FT PROPEP 20 213 POTENTIAL.

FT CHAIN 214 435 METALLOPROTEINASE.

FT CHAIN 456 550 DISINTEGRIN.

FT DOMAIN 20 672 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 673 696 POTENTIAL.

FT DOMAIN 697 748 CYTOPLASMIC (POTENTIAL).

FT ACT\_SITE 383 384 BY SIMILARITY (BY SIMILARITY).

FT METAL 383 383 ZINC (CATALYTIC) (BY SIMILARITY).

FT METAL 387 387 ZINC (CATALYTIC) (BY SIMILARITY).

FT METAL 393 393 ZINC (CATALYTIC) (BY SIMILARITY).

FT CARBOHYD 267 267 N-LINKED (GLCNAC) (BY SIMILARITY).

FT CARBOHYD 278 278 N-LINKED (GLCNAC) (BY SIMILARITY).

FT CARBOHYD 439 439 N-LINKED (GLCNAC) (BY SIMILARITY).

FT CARBOHYD 551 551 N-LINKED (GLCNAC) (BY SIMILARITY).

SEQUENCE 748 AA; 84188 MW; 202E2983061F9E1 CRG64;

Query Match 94.78; Score 3884.5; DB 6; Length 748;

Best Local Similarity 94.48; Pred. No. 0;

Matches 707; Conservative 19; Mismatch 22; Indels 1; Gaps 1;

DB 121 DQREGEFLQTHGGTFYVEPAERYIKDRTLPFHSVYIHEDDIKYPPKYGPOGGCADHSVFE 180

QY 181 RMKRYQMTGVEEGARAPPEKHAASGPELLRRKRTTLAERNTOCYLTOTDHLFFKYYGTR 240

DB 181 RRRKYQMTGVEEGARAPPEKHAASGPELLRRKRTTLAERNTOCYLTOTDHLFFKYYGTR 229

QY 241 EAVVAQTSNHAIDTLYOTDSSGIRNISPFWKRTIRITSSDEKOPNPRFNIIVEK 300

DB 240 EAVVAQTSNHAIDTLYOTDSSGIRNISPFWKRTIRITSSDEKOPNPRFNIIVEK 299

QY 301 FLEINSEONHDYCLAVVFDPRDGVGLAWVGPSSSGGICENKSLSDCKKSLN 360

DB 300 FLEINSEONHDYCLAVVFDPRDGVGLAWVGPSSSGGICENKSLSDCKKSLN 359

QY 361 TGLITVQYVGSHPVPPKSHITFAHEVGNHFGSPHDSGIECTPGESKNIGOKENYIMYA 420

DB 360 TGLITVQYVGSHPVPPKSHITFAHEVGNHFGSPHDSGIECTPGESKNIGOKENYIMYA 419

QY 421 RATSQDKLNKKFSLCSIRNISQVLEKRRNCFVBSQPCICGNCWEDEGDCDGSYDQC 480

DB 420 RATSQDKLNKKFSLCSIRNISQVLEKRRNCFVBSQPCICGNCWEDEGDCDGSYDQC 479

QY 481 KDCQCFDANOPEGKCKLKRGKOCSPSGPCTAHCAFEKSTREKCRDSDCAKEGICNGI 540

DB 480 KDCQCFDANOPEGKCKLKRGKOCSPSGPCTAHCAFEKSTREKCRDSDCAKEGICNGI 539

QY 541 TALCPASDPKPNFTDCNRHTQVCINGOCAGSICENYDLECTCASSDCKNKEICHYCCM 600

DB 540 TALCPASDPKPNFTDCNRHTQVCINGOCAGSICENYDLECTCASSDCKNKEICHYCCM 599

QY 601 KKMPSGTCASGSIOWSKGSPGRTITLPGSPCNPFCYGVPMNCRVYDADGLATLKK 660

DB 600 KKMPSGTCASGSIOWSKGSPGRTITLPGSPCNPFCYGVPMNCRVYDADGLATLKK 659

QY 661 AIFSPQYENIAEWIVAHMVAVLMGIALIMAGRIKICSVHPSSNPKLPPEKPLPGT 720

DB 660 AIFSPQYENIAEWIVAHMVAVLMGIALIMAGRIKICSVHPSSNPKLPPEKPLPGT 719

QY 721 LKRRRPOPIDQPPORHRESYOMGHMR 749

DB 720 LKRRRPOPIDQPPORHRESYOMGHMR 748

RESULT 4

ID 010742 PRELIMINARY: PRT: 691 AA.

AC 010742: 092650;

DT 01-NOV-1996 (TREMBLER, 01, Created)

DT 01-JAN-1998 (TREMBLER, 05, Last sequence update)

DE 01-JUN-2001 (TREMBLER, 17, Last annotation update)

DE DISINTEGRIN-METALLOPROTEASE MAMM (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96276398; PubMed=8694785;

RA Howard L., Lu X., Mitchell S., Griffiths S., Glynn P.;

RT "Molecular cloning of MAMM: a catalytically active mammalian disintegrin-metalloprotease expressed in various cell types.";

RT Biochem. J. 317:45-50(1996).

CC EMBL: Z48579; CAAB8463.1; -.

DR HESP; P18619; IFLV.

DR MERO; M12.210; -.

DR InterPro: IPR001762; Disintegrin.

DR InterPro: IPR001590; Repolysin.

DR InterPro: IPR000130; Zn\_MTPeptide.

DR Pfam: PF00200; disintegrin\_1.

DR Pfam: PF01421; Repolysin; 1.

DR PRINTS; PR00289; DISINTEGRIN.

DR SMART; SM00050; Disin; 1.

DR PROSITE; PS50215; ADAM\_MERO; 1.

DR PROSITE: PS50214; DISINTEGRIN\_2; 1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
 KM INTEGRIN.  
 FT NON\_TER  
 SQ SEQUENCE 691 AA; 77632 MW; 884369872486B292 CRC64;

Query Match 81.6%; Score 3346; DB 4; Length 691;  
 Best Local Similarity 88.4%; Pred. No. 4,5e-264;  
 Matches 612; Conservative 16; Mismatches 12; Indels 52; Gaps 2;

DR 109 GEGSSSHGVSVDGREGIKRGFTIEPAERYIKDRILPFIHSYVHEDDIN-----162  
 DB 1 GEGSSSHGVSVDGREGIKRGFTIEPAERYIKDRILPFIHSYVHEDDIN-----162  
 QY 163 -----YPAHYGPGGCADHS 177  
 DB 61 LRKLMSLELTSCCLPCALLHSMKKAVNSHCLYFKDPWGPSEIYYPHKXPGGCGADHS 120  
 QY 178 VFERMRKYQMTGVEEGARHPKHAASSCPPELLKKRTTLAERTCOLYIQTHLFEKTY 237  
 DB 121 VFERMRKYQMTGVEEYQIPEEHAA-NGPELLKKRTTSEKTCOLYIQTHLFEKTY 179  
 QY 238 GTRBAVIAQISSHVKAIDITYQTFDSGIRNISPMVKRIRINTSDEKPTNFRPNIG 297  
 DB 180 GTRBAVIAQISSHVKAIDITYQTFDSGIRNISPMVKRIRINTADEKPTNFRPNIS 239  
 QY 298 VERFLELNSQNNDDYCLAYVFTDRDQVYGLAVNGARSGSSGCIKSKISYSGKKK 357  
 DB 240 VERFLELNSQNNDDYCLAYVFTDRDQVYGLAVNGARSGSSGCIKSKISYSGKKK 299  
 QY 358 SLMTGIIYQNVGSHVPRKVSHTFAHEVGHNFSGPHDSGTECPGSEKMIJQKENGNY 417  
 DB 300 SLMTGIIYQNVGSHVPRKVSHTFAHEVGHNFSGPHDSGTECPGSEKMIJQKENGNY 359  
 QY 418 MYKARSQKLNKNSKLSINISQVLEKRNCFESOPICGNMVGEGECGCGS 477  
 DB 360 MYKARSQKLNKNSKLSINISQVLEKRNCFESOPICGNMVGEGECGCGS 419  
 QY 478 DQKDCDCEPDANPEGRKCKLPRKQCSPSQPCCTACQAFKSKSEKCRDSDCAEKGIC 537  
 DB 420 DQKDCDCEPDANPEGRKCKLPRKQCSPSQPCCTACQAFKSKSEKCRDSDCAEKGIC 479  
 QY 538 NGFTALCPASDPKPNFTDQNRHTQVINGCAGSICEKYDEECTCASSGCKNKKLCHV 597  
 DB 480 NGFTALCPASDPKPNFTDQNRHTQVINGCAGSICEKYDEECTCASSGCKNKKLCHV 539  
 QY 598 CCKKMAFSTCASTGSLQWSKQSGRTTLPQSPCNDFRQCDYFMRCLVDADGPLAR 657  
 DB 540 CCKKMAFSTCASTGSLQWSKQSGRTTLPQSPCNDFRQCDYFMRCLVDADGPLAR 599  
 QY 658 LKRAISPOLYENIAEYIAHMAVILMGITLIMMAGFKICSVHPSSNPPLPPPKL 717  
 DB 600 LKRAISPOLYENIAEYIAHMAVILMGITLIMMAGFKICSVHPSSNPPLPPPKL 659  
 QY 718 PGTLLRRRPPQIOPQPPROPRESYOMGMRR 749  
 DB 660 PGTLLRRRPPQIOPQPPROPRESYOMGMRR 691  
 RESULT 5  
 Q10743 PRELIMINARY: PRT: 544 AA.  
 AC Q10743;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE DISINTEGRIN-METALLOPROTEASE PRECURSOR (EC 3.4.24.-) (MELIN-ASSOCIATED METALLOPROTEINASE) (MADM) (FRAGMENT).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;

RN SEQUENCE FROM N.A.  
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;  
 RX MEDLINE-96276398; PubMed-9694785;  
 RA Howard L., Mitchell S., Lu X., Griffiths S., Glynn P.;  
 RT "Molecular cloning of MADM: a catalytically active mammalian  
 protein disintegrin-metalloprotease expressed in various cell types";  
 RL Biochem. J. 317:45-50(1996).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28 (ZINC  
 CC METALLOPROTEINASE); ALSO KNOWN AS THE REPROLYSIN SUBFAMILY.  
 CC -1- SIMILARITY: HIGH, IN THE MIDDLE REGION, TO DISINTEGRINS.  
 DR EMBL: Z48444; CA48359.1; ..  
 DR HSSP: P18619; IFLV.  
 DR MEROPS: M2.210; ..  
 DR InterPro: IPR001762; Disintegrin.  
 DR InterPro: IPR001590; Reprolysin.  
 DR InterPro: IPR000130; Zn.MTpeptase.  
 DR Pfam: PF00200; disintegrin; 1.  
 DR Pfam: PF01421; Reprolysin; 1.  
 DR PRINTS: PR00289; DISINTEGRIN.  
 DR SMART: SM00050; DISIN.  
 DR PROSITE: PS50215; ADAM\_MEPRO; 1.  
 DR PROSITE: PS50214; DISINTEGRIN\_2; 1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
 KM Integrin; Hydrolase; Metalloprotease; Transmembrane; Zinc; Signal;  
 KW Glycoprotein.  
 FT NON\_TER 1 1  
 FT SIGNAL <1 9  
 FT CHAIN 10 241 METALLOPROTEINASE.  
 FT CHAIN 242 346 DISINTEGRIN.  
 FT DOMAIN 10 468 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 469 492 POTENTIAL.  
 FT DOMAIN 493 544 CYTOPLASMIC (POTENTIAL).  
 FT ACT\_SITE 180 180 BY SIMILARITY.  
 FT METAL 179 179 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT METAL 183 183 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT METAL 189 189 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 544 AA; 60444 MW; F75E08BD6C8A7DD CRC64;  
 Query Match 72.0%; Score 2956; DB 11; Length 544;  
 Best Local Similarity 98.5%; Pred. No. 1,9e-232;  
 Matches 536; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
 QY 206 GPELARKKKTTLAEANTCOLYIQTHLFPKYVGRBAVIAQISSHVKAIDITYQTFDESG 265  
 DB 1 GPELARKKKTTLAEANTCOLYIQTHLFPKYVGRBAVIAQISSHVKAIDITYQTFDESG 206  
 QY 266 IIRISPMVKRIRINTSDEKPTNFRPNIGYKRELINSQNNDDYCLAVFTDRFD 325  
 DB 61 IIRISPMVKRIRINTSDEKPTNFRPNIGYKRELINSQNNDDYCLAVFTDRFD 120  
 QY 326 DGYLGLAWGAPSGSSGCIKSKISYSGRTTLPQSPCNDFRQCDYFMRCLVDADGPLAR 385  
 DB 121 DGYLGLAWGAPSGSSGCIKSKISYSGRTTLPQSPCNDFRQCDYFMRCLVDADGPLAR 326  
 QY 386 VGHNGSPHDSGTECPGSEKMIJQKENGNYIMYARATSGDKLNKNSKLSIRNISQV 445  
 DB 181 VGHNGSPHDSGTECPGSEKMIJQKENGNYIMYARATSGDKLNKNSKLSIRNISQV 386  
 QY 446 EKKRNKCFESOPICGNMVGEGECDCGYSPQCDPCPDANPEGRKCKLPRKQCS 505  
 DB 241 EKKRNKCFESOPICGNMVGEGECDCGYSPQCDPCPDANPEGRKCKLPRKQCS 446  
 QY 506 PSQGPCCTACQAFKSKSEKCRDSDCAKEGIFALCPASDPKPNFTDQNRHTQVGIN 565  
 DB 301 PSQGPCCTACQAFKSKSEKCRDSDCAKEGIFALCPASDPKPNFTDQNRHTQVGIN 506



QY 618 KQSGRTTLPQSPCNDPFGYCDVPMRCRLVDADGPLARLTKAIFSPOLYENIAEWYA 677  
 DB 849 YNIOKGGISLQPSGPDNDPQGYCDVFLKCAVADADGFLMLKMLNKRKLQVYAEWYD 908  
 QY 678 HMMVLLMGIALIMLAGFIKCSVHPSSNPKLPPLPGTLK-----RRRPPPIQ 731  
 DB 909 NMYLVLMGVAFIYVMGSIKCAVHPSSNPKRRARRISETILRAVMYTLFRMGRHPNQ 968  
 QY 732 Q--PPROPRESYOMGHMR 749  
 DB 969 RGAGPRISIPPAHEAOHYSR 988

RESULT 7  
 Q94902 PRELIMINARY; PRT; 1239 AA.  
 AC Q94902;  
 DT 01-FEB-1997 (TREMBLrel. 02, Created)  
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE KUZBANIAN.  
 GN KUZ OR BG:DS07660.3 OR CG7147.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NC NCBITaxid=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96355647; PubMed=8703057;  
 RA Roake J., Pan D., Xu T., Rubin G.M.;  
 RT "Kuz, a conserved metalloprotease-disintegrin protein with two roles  
 in Drosophila neurogenesis.";  
 RL Science 273:1227-1231(1996).  
 DR EMBL: U60591; AAC47275.1; .  
 DR HSP: P17494; 1KST.  
 DR MEKOPS; M12.211; .  
 DR FlyBase: FBgn015954; kuz.  
 DR InterPro: IPR001762; Disintegrin.  
 DR InterPro: IPR001590; Reprolysin.  
 DR InterPro: IPR00130; zn\_MpPepIdse.  
 DR SMART: SM00050; DISIN: 1.  
 DR PROSITE: PSS0215; ADAM\_MERO: 1.  
 DR PROSITE: PSS0214; DISINTEGRIN\_2; 1.  
 DR PROSITE: PSS0142; ZINC\_PROTEASE; UNKNOWN\_1.  
 DR Neurogenesis.  
 SQ SEQUENCE 1239 AA; 136522 MW; 7FCB514A1352577A CRC64;

Query Match 36.3%; Score 1489; DB 5; Length 1239;  
 Best Local Similarity 34.4%; Pred. No. 1, 9e-112;  
 Matches 337; Conservative 131; Mismatches 267; Indels 246; Gaps 22;

QY 7 LILLISMAAGLG-OTGNP-LNKYIRHESLSTYVDSLHOKHOKRAVSHEDQILLDF 64  
 DB 17 IIVNCGVADISGVKGRHERLNEYSHYETLNYDHEIRASHNRARSYT-KQYVHLRF 75  
 QY 65 HAIGROFNLMKRDSTLSEDFKVFYSNKVLVDYTSIYGHYIGEGSGSHSDVGRF 124  
 DB 76 ASHGROFHLKRDNLNFTSNKLDYDSKPIDVSTDIHYGEYIGDRNSVFSINGVF 135  
 QY 125 EGIKTRGGTFYTERPARY----- 144  
 DB 136 EGIITRDVAYVEHAKHYFPTNRTATTPSTSTSSATVTKSTQTPRLAKSNSTYT 195  
 QY 145 -----KDR-----LLPFH 152  
 DB 196 AVNSKRNFIKIASTTTSOOLPEYTSSTSSSTTTPPTTEYFEDKERNADDELDPH 255  
 QY 153 SVIY---HEDDINYPKHYGPOGCA-----DHSYFERNR 183  
 DB 256 SIYKSHVEDAYENYREGVAGGIDTDEVQSOMMENIONSVAEELPEPMSKDYQKILHRQ 315

QY 184 KYOMTGVESGARAPHERHAASSG-----PELLKKRRRTLAE----- 219  
 DB 316 LHKSAPOQOQPPHPPKYISGDEDFYPHQKTKKANPAECAFDPSTGRRLOSSANVA 375  
 QY 220 -----RNTQLYIQTDLFFKYY----- 237  
 DB 376 DMHQLVHRVRATDNCAGDRSGSGSGRGRENKNTCSLYIQTPLIMRIREGIADHD 435  
 QY 238 -----GTREAVIAQISSHVAKIDTYOTDFSG---TANISPMVKRIIRINTS--- 282  
 DB 436 RGKRYEVDKTRRELTSLIAHYAVNY IYRNKTFGGRTEHNRNINEYQRIKIDDSCKR 495  
 QY 283 -DEKPTNPPRPNIGVEKFLNSEQNHDDYCLAYFTDPDQVGLAMVAGPSSG 341  
 DB 496 NSYNGPRHNAFCNEHMDVSNFLNLHSLDHSDFCLAYFTYRDTGTTGLAMVASAGAS 555  
 QY 342 GGICEKSKLYSD-----GKKSLNLTGITTVOYNSHVPVPSHITPFAHEGHNFSPH 394  
 DB 556 GGICEKTYTETVQGYQSTRSLNTGILTFPNVYSKRPVYSQTLAHEIGHNFSPH 615  
 QY 395 DSGTECTPGESKNLGQKENGNYIMYARATSGDKLNNKFTSLCSIRNISQVLE---KRN 450  
 DB 616 DYPOECRPGSL-----NGNYIMFASATISGDRPNNSKSPSISINISNVLVDLYVGNTR 668  
 QY 451 NCFVESGDPICNGVBEQECDCGYS-DQCKDDCF-----DANQPECKCKLPG 501  
 DB 669 DCFKASGAFPGCKKIVBSGEBDCGFMEECKKCCYPLIJEYQSLNSSAKGCTRAK 728  
 QY 502 KCCSPSGQPCCTA-QCAF--KSKSEKCRDSDCAKAGICNGFTALCPASDPKPNFTDNR 558  
 DB 729 TCCSPSGQPCCTSNCTFTVPYSYHQCKETECSSMSSTNGTTACCPERRHRDRTKMN 788  
 QY 559 HHQVINCOCAGSICEKEDLEEC--TCASDQKNEILCHVCMKMAPSHCASTGSLQW 616  
 DB 789 GTALCTRCGCSGSLMLNMKICLSTIPIHYSKRLKLDLACQGNQNTSICRSTSEAD 848  
 QY 617 SKQSGRTITLQPSGPNDRPGYCDVPMRCRLVDADGPLARLTKAIFSPOLYENIAEWY 676  
 DB 849 KYNIOKGGISLQPSGPDNDPQGYCDVFLKCAVADADGFLMLKMLNKRKLQVYAEWY 908  
 QY 677 HMMVLLMGIALIMLAGFIKCSVHPSSNPKLPPLPGTLK-----RRRPPPI 730  
 DB 909 NMYLVLMGVAFIYVMGSIKCAVHPSSNPKRRARRISETILRAVMYTLFRMGRHPN 968  
 QY 731 QO--PPROPRESYOMGHMR 749  
 DB 969 RGAGPRISIPPAHEAOHYSR 988

RESULT 8  
 Q94902 PRELIMINARY; PRT; 1236 AA.  
 AC Q94902;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE KUZ PROTEIN.  
 GN KUZ OR BG:DS07660.3 OR CG7147.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NC NCBITaxid=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=Y, CN BW SP;  
 RX MEDLINE=99403001; PubMed=10471707;  
 RA Ashburner M., Misra S., Roake J., Lewis S.E., Blazek R., Davis T.,  
 RA Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,  
 RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Mostreli A.,  
 RA Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitehaw K.,  
 RA Celinker S., Rubin G.M.;  
 RT "An exploration of the sequence of a 2.9-Mb region of the genome of









Best Local Similarity 25.4%; Pred. No. 2,6e-25;  
Matches 165; Conservative 98; Mismatches 263; Indels 123; Gaps 34;

9 LLSM--AAGCG---QYGNPKYTHHYGLSYNDVSHQHNKRAVSHEDOFLLD 63  
12 LRLMLAGGLGVLGAGRDLEQVYHLS--SYELITWRLRRRRALPSSQSLSYV 69  
64 FNAHGFNLMMKRDTSLSDFDEKVFETSNK---VLDYDT--SHI-YTHGYGEESFSH 116  
70 IOAGGKOHILHLENTDLLPNDFVYTYDEKESLSDHNVNOSHCHGYEGVQNSVA 129  
117 GSVIDREGFIRKRGFTYTPAEKRIKDRILPFHSVYIHEDDINTYHKKGPGGCGADH 176  
130 VSACG-LRGLHLHNASFGIEPLHNSH---FEHIFPMGDI--HQEPLKGVSNR 180  
177 SVFERMRKYOMTVEEGARAHPEKHAASGPELLRRKRTTLAERTCOLYQTDHLEPKY 236  
181 DT-----EKEGTGDEEH--PSVQLRRRAVLPQTYVELFIVYKERDM 227  
227 YGTRF-AVIAQISSHVKADITQYTFDSGIRNISPMVKRINTTSEKOPTNPFPRN 295  
228 MGRNQTAVREEMITLANTLDSMT-----MLNRIYLVGLEIMT--DRNPINIGAG 278  
296 IGEKEFLD---LNSQNDHDCYAVFTDRDQDGLVGLAMVAPSGSSGQICEKSL 350  
279 DVLGNFYQMRREKFLITRRHDS---AQLYLKGF--GGTGMAFVGT-----YCSRS-- 325  
351 YSDGKKKSLNT-GIITVONGSHVPRVSHITFAHVEGNHNSPDSGTECPESKRLG 409  
326 HMG---INVFQITVETFASTV-----AHELGNILMNHDDERECFCAR--- 368  
410 OKENGNTYMARATSGDKLNKNSLCSIRNISQVLEKRNCFVE-----SGOPTCG 462  
369 -----SCIMNSGAS-----GSRNFSSCAEDFEKILTLNKGSGCLINTIPKPEAVSAPCG 418  
463 NCMVQEGECGCGYSDCK--DCCFDANQPEGKKCKLKKGKCSOSOPCTACAKRSK 521  
419 NKLVDPGECCCGGAKCEVDPC-----EGSTCKLKSFAEC--AYDCC-KDCQELPG 469  
522 SEKCR-DDSDCAKEGICNGFTALCPASDPKPNFTDCNRHTOYCINGGAGSICEKYLEE 580  
470 GSMCKGTSECDVPEYCNSSGSOFCPPDVFIONGYPCQNSKACVANG-----MCQYADQ- 523  
581 CTCASDCKDKNELCHYCCMKMAP-----STCASGSLGMSKQSGRTI 625  
524 --CQYIRSKAKAPRCFIEVNSKQDRGNCQFSGS-EYKRCATGNAL 569

RESULT 14  
Q9PVK7 PRELIMINARY; PRT; 600 AA.  
ID Q9PVK7;  
DT 01-MAY-2000 (TREMblrel. 13, Created)  
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
DE COBRIN PRECURSOR.  
OS Najia naja (Indian cobra).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;  
OC Elapidae; Elapinae; Najia.  
OX NCBI\_Taxid=35670;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=KAUTHIN; TISSUE=VENOM GLAND;  
RA Bamba B., Bredehorst R., Vogel C.-W.;  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
DR HSSP; P17494; 1KSF.  
DR InterPro: IPR001762; Disintegrin.  
DR InterPro: IPR002870; Pep.M2B-prop.  
DR InterPro: IPR001590; Repolysin.  
DR InterPro: IPR001330; Zn-MTPeptide.  
DR Pfam; Pf00200; disintegrin; 1.

DR Pfam; PF01563; Rep.M2B-prop; 1.  
DR Pfam; PF01421; Repolysin; 1.  
DR PRINTS; PR00289; Disintegrin.  
DR ProDom; PD000664; Disintegrin; 1.  
DR SMART; SM00050; Disin; 1.  
DR PROSITE; PS50215; ADAM MEPR; 1.  
DR PROSITE; PS50214; DISINTEGRIN; 2; 1.  
DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
KV SIGNAL.  
FT SIGNAL 1 6 POTENTIAL.  
FT CHAIN 180 600 COBRIN.  
SQ SEQUENCE 600 AA; 67661 MW; C7C0D45EBC694290 CRC64;

Query Match 10.0%; Score 409; DB 13; Length 600;  
Best Local Similarity 24.1%; Pred. No. 6,8e-25;  
Matches 156; Conservative 97; Mismatches 238; Indels 156; Gaps 31;

47 QAKRAVSHEDOFLLDFAHGFNLMMKRDTSLSDF-----KVFETSNK 96  
36 QNPQPEKYEEDT-MQYEFVQNPCEPVVHLERNKGLFSDYETRYAPDGRITTSPPVQD 94  
97 YDTHIYTHGYEGESFSGSYIDREFCFIKTGGFYTPAEKRIKDRILPFHSVYI 156  
95 H---CYHGFQPNADSANVYSACDS-LKGHFKLOGELIYFIEPLK--ISDS--EANA-IV 145  
157 HEDDINTPKHYGPOGGCASHVEFRMRKYQMTGVEEGARAHPEKHAASGPELLRRKRTT 216  
146 KDENEVEDETFPKIGQVTD-TWESDEPIKRTSL-----LTPNPE--DQRYL 189  
217 LAERNFCOLYQTDHLEFFKYGFRRAVI-AQISSHVKADITQYTFDSGIRNISPMVKR 275  
190 QAER-YIEFYMYVDNIMTRYKKNQVLYRKRYEIMNMNITRYLNF-----HIALIGLE 244  
276 I-----KINTSDEKOPTNFERPPNIGVEKFLNELSDQNDHDCYAVFTDRDQDGLG 330  
245 IWSNINELNVOQVKAETLDF-----GEWEREKLLPFRNRDN--AQLTLGIDFNGPRVG 296  
331 LAWYGAPSGSSGGICEKSKLYSDGKKSLNTGIIYQVNGSHVPRVSHITFAHVEGNHNF 390  
297 LAYIGS-----ICNP-----KTSAAVQDYKST--RMVAITMAHEGHNH 335  
391 GSPHDSGTECPESKRLNLOGKENGNTIMYARATSGDKLNKNSLCSIRNISQVLEKRR 450  
336 GMINDKGF-CTCGPRN-----CVMSTRRTK---PAYOFSSGVRHQRLLLRDP 381  
451 NCFVES-----QPPICGNGVQEGEEDCGYSDCKDCCFDANQPEGKKCKLKPRQ 503  
382 QCLNKPLSTDIIVSPICGNYFEVGEEDCGSPADCGSACC-----NATPCKLIHQEAQ 435  
504 CSPSGCCCTAOCAPFKSSEKGR-DDSDCAKEGICNGFTALCPASDPKPNFTDCNRHTOY 562  
436 CDSE-----CEKCKFKGAGAECAKADCDLPELCTGASACPPDVFQORGLPC-QNNGY 491  
563 CINGQC-----AQSICEKYDLEECTCASSDCKDK 592  
492 CYNKCPIMTNOCIALRGVYKVRSDCPTLQMTFRGGICLRMEYGRKIPCAKADVKCR 551  
593 ELC-----HYCCMKMAPSTCASGSLGMSKQSGRTITLQGSGCND 635  
552 LFCCKRNSMTCNCISPRD-PSIG-----NVEGTGCGD 584

RESULT 15  
ID 077633 PRELIMINARY; PRT; 75 AA.  
AC 077633;  
DT 01-NOV-1998 (TREMblrel. 08, Created)  
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)  
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
DE DISINTEGRIN-METALLOPROTEINASE PRECURSOR (FRAGMENT).  
GN ADAM-10.  
OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OX Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Flannery C.R., Little C.B., Caterson B., Hughes C.E.;  
 RT "Expression of articular cartilage metalloproteinases by chondrocytes  
 in fresh tissue and explant, monolayer and agarose cultures.";  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF069645; AAC23529.1; -.  
 DR MEROPS; M12.210; -.  
 DR InterPro; IPR001590; Reprolysin.  
 DR PROSITE; PS50215; ADAM\_MERPRO; 1.  
 KW Integrin.  
 FT NON\_TER 1 1  
 FT NON\_TER 75 75  
 SO SEQUENCE 75 AA; 8224 MM; C03B70C901333557 CRC64;

Query Match 9.9%; Score 406; DB 6; Length 75;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-26;  
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 393 PHDSGTECPGSGSKNLGKENGNTYMYRATSGDKLNNKFSLCSIRNISQYLEKKRNNC 452  
 Db 1 PHDSGTECPGSGSKNLGKENGNTYMYRATSGDKLNNKFSLCSIRNISQYLEKKRNNC 60  
 OY 453 FVSGQPICGNGMVE 467  
 Db 61 FVSGQPICGNGMVE 75

Search completed: April 1, 2002, 15:12:14  
 Job time: 696 sec